

CAA04703.1	AJ001370	Olea europaea	cytochrome b5. cytb5-2.
AAA32990.1	M87514	Brassica oleracea	cytochrome b-5. cytochrome b-5.
CAA50575.1	X71441	Nicotiana tabacum	cytochrome b5.
CAA53366.1	X75670	Oryza sativa	cytochrome b5.
CAA04702.1	AJ001369	Olea europaea	cytochrome b5. cytb5-1.
AAA62621.1	L22209	Cuscuta reflexa	associated with cytokinin-induced haustoria formation in Cuscuta reflexa. cytochrome b5.
AAC49701.1	U79011	Borago officinalis	haem-binding protein. cytochrome b5.
CAA56318.1	X80008	Nicotiana tabacum	cytochrome b5.
CAA48240.1	X68140	Nicotiana tabacum	cytochrome b5.
AAD10774.1	AF098510	Petunia x hybrida	involved in anthocyanin biosynthesis. cytochrome b5 DIF-F. diff. required for full activity of flavonoid 3',5' hydroxylase.
AAF60299.1	AF233640	Petunia x hybrida	involved in anthocyanin biosynthesis. cytochrome b5 DIF-F. diff.
CAA11033.1	AJ222981	Physcomitrella patens	delta6-acyl-lipid desaturase. des6. des6 represents a fusion between a C-terminal desaturase with a cytochrome b5-related part and a N-terminal extension.
SEQ ID NO: 392			
AAK28303.1	AF346431	Nicotiana tabacum	phenylpropanoid:glucosyltransferase 1. togt1. glucosyltransferase.
AAB36653.1	U32644	Nicotiana tabacum	immediate-early salicylate-induced glucosyltransferase. IS5a.
BAB17061.1	AP002523	Oryza sativa	putative glucosyl transferase. P0013F10.7. contains EST C73149(E2992).
AAB36652.1	U32643	Nicotiana tabacum	immediate-early salicylate-induced glucosyltransferase. IS10a.
AAK28304.1	AF346432	Nicotiana tabacum	phenylpropanoid:glucosyltransferase 2. togt2. glucosyltransferase.
BAB17059.1	AP002523	Oryza sativa	putative glucosyl transferase. P0013F10.5.
BAB17060.1	AP002523	Oryza sativa	putative glucosyl transferase. P0013F10.6.
CAA59450.1	X85138	Lycopersicon esculentum	twil. homologous to glucosyltransferases.

CAB56231.1	Y18871	<i>Dorotheanthus bellidiformis</i>	betanidin-5-O-glucosyltransferase.
BAA83484.1	AB031274	<i>Scutellaria baicalensis</i>	UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.
AAB48444.1	U82367	<i>Solanum tuberosum</i>	UDP-glucose glucosyltransferase.
BAA36410.1	AB012114	<i>Vigna mungo</i>	UDP-glycose:flavonoid glycosyltransferase. UFGlyT.
CAA54610.1	X77460	<i>Manihot esculenta</i>	UTP-glucose glucosyltransferase. CGT4.
CAB88666.1	AJ400861	<i>Cicer arietinum</i>	flavonoid glycosyltransferase. putative UDP-glycose.
AAK16180.1	AC079887	<i>Oryza sativa</i>	putative glucosyltransferase. OSJNBa0040E01.21.
AAD51778.1	AF116858	<i>Phaseolus vulgaris</i>	utilizes UDPX as the sugar donor and catalyzes the formation of O-xylosylzeatin from zeatin. zeatin O-xylosyltransferase. ZOX1.
AAD04166.1	AF101972	<i>Phaseolus lunatus</i>	catalyzes formation of O-glucosylzeatin from zeatin and UDPG; catalyzes formation of O-xylosylzeatin from zeatin and UDPX. zeatin O-glucosyltransferase. ZOG1. cytokinin O-glucosyltransferase.
BAA89009.1	AB027455	<i>Petunia x hybrida</i>	anthocyanin 5-O-glucosyltransferase. PH1.
CAC09351.1	AL442007	<i>Oryza sativa</i>	putative glucosyltransferase. H0212B02.7.
AAB62270.1	AF006081	<i>Solanum berthaultii</i>	UDPG glucosyltransferase. PLGT.
AAK16172.1	AC079887	<i>Oryza sativa</i>	putative glucosyltransferase. OSJNBa0040E01.14.
AAF61647.1	AF190634	<i>Nicotiana tabacum</i>	UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.
CAA54612.1	X77462	<i>Manihot esculenta</i>	UTP-glucose glucosyltransferase. CGT5.
AAK16181.1	AC079887	<i>Oryza sativa</i>	putative glucosyltransferase. OSJNBa0040E01.16.
AAK16178.1	AC079887	<i>Oryza sativa</i>	putative glucosyltransferase. OSJNBa0040E01.5.
BAA36412.1	AB012116	<i>Vigna mungo</i>	UDP-glycose:flavonoid glycosyltransferase. UFGlyT.
AAK16175.1	AC079887	<i>Oryza sativa</i>	putative glucosyltransferase. OSJNBa0040E01.15.

-
- AAF98390.1 AF287143 *Brassica napus*
catalyzes the transfer of glucose from UDP-glucose to sinapate and some other hydroxycinnamates (4-coumarate, caffeate, ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.
-
- BAA36423.1 AB013598 *Verbena x hybrida*
UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.
-
- AAF17077.1 AF199453 *Sorghum bicolor*
UDP-glucose glucosyltransferase. UDP-glucose:p-hydroxymandelonitrile-o-glucosyltransferase.
-
- BAA93039.1 AB033758 *Citrus unshiu*
limonoid UDP-glucosyltransferase. LGTase.
-
- BAB17176.1 AP002843 *Oryza sativa*
putative UTP-glucose glucosyltransferase. P0407B12.13.
-
- BAB17182.1 AP002843 *Oryza sativa*
putative UTP-glucose glucosyltransferase. P0407B12.19.
-
- BAA89008.1 AB027454 *Petunia x hybrida*
anthocyanidin 3-O-glucosyltransferase. PGT8.
-
- CAA54558.1 X77369 *Solanum melongena*
glycosyl transferase. GT.
-
- CAA54611.1 X77461 *Manihot esculenta*
UTP-glucose glucosyltransferase. CGT2.
-
- CAA54609.1 X77459 *Manihot esculenta*
UTP-glucose glucosyltransferase. CGT1.
-
- BAA12737.1 D85186 *Gentiana triflora*
UDP-glucose:flavonoid-3-glucosyltransferase.
-
- AAD21086.1 AF127218 *Forsythia x intermedia*
adds glucose residue to position 3 of flavonoid compounds. flavonoid 3-O-glucosyltransferase. UFGT.
-
- AAG25643.1 AF303396 *Phaseolus vulgaris*
UDP-glucosyltransferase HRA25. putative; defense associated.
-
- BAA36411.1 AB012115 *Vigna mungo*
UDP-glucose:flavonoid glycosyltransferase. UFGlyT.
-
- BAA19155.1 AB000623 *Nicotiana tabacum*
glucosyl transferase. JIGT.
-
- AAD55985.1 AF165148 *Petunia x hybrida*
catalyzes the penultimate step of flavonol glucosylgalactoside biosynthesis from UDP-galactose and flavonol aglycones in petunia pollen. UDP-galactose:flavonol 3-O-galactosyltransferase. F3galtase.
-
- CAA54613.1 X77463 *Manihot esculenta*
UTP-glucose glucosyltransferase. CGT6.
-
- BAA36421.1 AB013596 *Perilla frutescens*
UDP-glucose:anthocynin 5-O-glucosyltransferase. PF3R4.
-

BAA19659.1	AB002818	<i>Perilla frutescens</i> flavonoid 3-O-glucosyltransferase. UDP glucose.
AAB81683.1	AF000372	<i>Vitis vinifera</i> UDP glucose:flavonoid 3-o-glucosyltransferase.
BAB41025.1	AB047098	<i>Vitis vinifera</i> UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT1.
BAB41023.1	AB047096	<i>Vitis vinifera</i> UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT1.
SEQ ID NO: 393		
CAB56756.1	AJ011589	<i>Pisum sativum</i> 5,10-methylenetetrahydrofolate dehydrogenase: 5,10-methenyltetrahydrofolate cyclohydrolase. bifunctional enzyme.
AAD01907.1	AF030516	<i>Pisum sativum</i> 5,10-methylenetetrahydrofolate dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase. bifunctional protein; 31.3 kDa protein.
AAG48834.1	AC084218	<i>Oryza sativa</i> similar to <i>Pisum sativum</i> methylenetetrahydrofolate dehydrogenase (NADP+) (EC 1.5.1.5) (AF030516).
SEQ ID NO: 406		
AAD46491.1	AF135014	<i>Zea mays</i> dihydrolipoamide S-acetyltransferase. pyruvate dehydrogenase complex E2 subunit.
BAA90623.1	AP001129	<i>Oryza sativa</i> ESTs AU033004(S0924),C74754(E50863) correspond to a region of the predicted gene.; Similar to Rat mRNA for dihydrolipoamide acetyltransferase. (D10655).
BAA77024.1	AB026124	<i>Lithospermum erythrorhizon</i> dihydrolipoamide acetyltransferase.
SEQ ID NO: 407		
AAF69017.1	AF261654	<i>Dianthus caryophyllus</i> ethylene-insensitive 3-like protein 1. EIL1. EIN3-like protein.
CAC09582.1	AJ298994	<i>Fagus sylvatica</i> gibberellic acid (GA3)-induced. ethylene insensitive (EIN3/EIL)-like transcription regulator. ein11.
AAG00419.1	AF247568	<i>Nicotiana tabacum</i> EIN3. component in ethylene signal transduction pathway.
SEQ ID NO: 408		
AAC15870.1	AF002016	<i>Cucurbita</i> sp. acyl CoA oxidase homolog.
AAF14635.1	AF202987	<i>Petroselinum crispum</i> acyl-CoA oxidase. ACO. peroxisomal acyl-CoA oxidase.
AAB67883.1	U66299	<i>Phalaenopsis</i> sp. 'True Lady' acyl-CoA oxidase homolog.

AAC32108.1	AF051203	<i>Picea mariana</i> acyl-CoA oxidase homolog. Sb06. similar to Phalaenopsis sp. acyl-CoA oxidase homolog encoded by GenBank Accession Number U66299.
CAA04688.1	AJ001341	<i>Hordeum vulgare</i> putative acyl-CoA oxidase.
BAB08201.1	AP002539	<i>Oryza sativa</i> ESTs AU056822(S20908), C26441(C12328), C28477(C61243) correspond to a region of the predicted gene. Similar to <i>Arabidopsis thaliana</i> putative acyl-coA dehydrogenase (AF049236).
BAA96762.1	AP002521	<i>Oryza sativa</i> ESTs AU056822(S20908), C26441(C12328), C28477(C61243) correspond to a region of the predicted gene. Similar to <i>Arabidopsis thaliana</i> putative acyl-coA dehydrogenase (AF049236).
CAB55555.1	AJ010946	<i>Pisum sativum</i> auxin binding protein (ABP44). abp44/ivdh. has both auxin binding capability and enzymatic activity; isovaleryl-CoA Dehydrogenase.
CAB55554.1	AJ010945	<i>Pisum sativum</i> auxin binding protein (ABP44). abp44/ivdh. has both auxin binding capability and enzymatic activity; Isovaleryl-CoA Dehydrogenase.
CAC08233.1	AJ278987	<i>Solanum tuberosum</i> leucine catabolism. isovaleryl-CoA dehydrogenase. ivd1.
CAC08234.1	AJ278988	<i>Solanum tuberosum</i> leucine catabolism. isovaleryl-CoA dehydrogenase. ivd2.
AAF02449.1	AF127432	<i>Picea abies</i> acyl-CoA oxidase homolog. Sb06.
AAF02451.1	AF127434	<i>Picea abies</i> acyl-CoA oxidase homolog. Sb06.
AAF02450.1	AF127433	<i>Picea abies</i> acyl-CoA oxidase homolog. Sb06.
AAC32152.1	AF051733	<i>Picea mariana</i> acyl-CoA oxidase homolog. Sb06.
AAC32153.1	AF051734	<i>Picea mariana</i> acyl-CoA oxidase homolog. Sb06.
CAA58874.1	X84055	<i>Hordeum vulgare</i> mammalian acyl CoA oxidase homologous. cdr29. putative.
SEQ ID NO: 409		
CAB64356.1	AJ251511	<i>Populus tremula</i> x <i>Populus tremuloides</i> mitochondrial oxidase. alternative oxidase. aox1.
AAC60576.1	S71335	Mitochondrion <i>Nicotiana tabacum</i> alternative oxidase. Aox1. This sequence comes from Fig. 1; AOX.
CAA56163.1	X79768	<i>Nicotiana tabacum</i> alternative oxidase. aox.
CAA48653.1	X68702	<i>Glycine max</i> alternative oxidase. aox1. putative.

AAC35354.1	AF083880	Glycine max	alternative oxidase precursor. Aox1. AOX1; terminal oxidase of mitochondrial electron transport chain.
BAB21500.1	AB055060	Catharanthus roseus	alternative oxidase.
BAA23803.1	AB009395	Catharanthus roseus	alternative oxidase.
BAA86963.1	AB007452	Oryza sativa	alternative oxidase. Aox1(Ao1-1).
BAA28773.1	AB004864	Oryza sativa	alternative oxidase. AOX1a.
BAA28772.1	AB004813	Oryza sativa	alternative oxidase. AOX1a.
CAA78823.1	Z15117	Sauromatum guttatum	salicylic acid-inducible alternative oxidase. aox1.
AAA34048.1	M60330	Sauromatum guttatum	alternative oxidase protein. aox1.
AAD51707.1	AF174004	Triticum aestivum	alternative oxidase.
CAA55892.1	X79329	Mangifera indica	alternative oxidase. AOMI 1.
CAB72441.1	AJ271889	Populus tremula x Populus tremuloides	mitochondrial oxidase. alternative oxidase. aox1b.
AAB97285.1	U87906	Glycine max	alternative oxidase. Aox2.
BAA28771.1	AB004813	Oryza sativa	alternative oxidase. AOX1b.
BAA28774.1	AB004865	Oryza sativa	alternative oxidase. AOX1b.
AAB97286.1	U87907	Glycine max	alternative oxidase. Aox3.
AAB97839.1	AF040566	Zea mays	alternative oxidase. Aox.
AAG33634.1	AF314255	Chlamydomonas reinhardtii	alternative oxidase 2. AOX2.
AAG02081.1	AF285187	Chlamydomonas reinhardtii	alternative oxidase. AOX2.
AAG33633.1	AF314254	Chlamydomonas reinhardtii	alternative oxidase 1. AOX1.
AAC05743.2	AF047832	Chlamydomonas reinhardtii	alternative oxidase. AOX1.
BAA23725.1	AB009087	Chlamydomonas sp. W80	alternative oxidase.

AAC34192.1 S81466 Glycine max
alternative oxidase Aox1 precursor. Aox1. This sequence comes from Fig. 1.

AAG18450.1 AF302932 Lycopersicon esculentum
plastid quinol oxidase.

AAG18449.1 AF302931 Lycopersicon esculentum
plastid quinol oxidase.

AAG02287.1 AF177980 Lycopersicon esculentum
plastid terminal oxidase. PTOX.

AAG02286.1 AF177979 Lycopersicon esculentum
plastid terminal oxidase. PTOX.

AAG02288.1 AF177981 Capsicum annum
plastid terminal oxidase. PTOX.

AAB36072.1 S81470 Glycine max
Aox2. Aox2. alternative oxidase 2; This sequence comes from Fig. 1.

AAC35554.2 AF085174 Oryza sativa
oxidase. IM1.

AAG00450.1 AF274001 Triticum aestivum
oxidase. IM1.

SEQ ID NO: 410

CAA69600.1 Y08292 Nicotiana plumbaginifolia
NADH glutamate dehydrogenase. GDH A.

CAB94836.1 AJ277949 Nicotiana plumbaginifolia
NADH glutamate dehydrogenase. gdhA.

CAC18730.1 AJ303070 Vitis vinifera
NADH glutamate dehydrogenase. gdhA.

CAA60507.1 X86924 Vitis vinifera
glutamate dehydrogenase. GDH.

BAA08445.1 D49475 Zea mays
glutamate dehydrogenase.

AAB51596.1 U93561 Zea mays
glutamate dehydrogenase. GDH1. wild type.

AAB51595.1 U93560 Zea mays
glutamate dehydrogenase mutant. GDH1. mutant allele.

CAB94837.1 AJ277950 Nicotiana plumbaginifolia
NADH-glutamate dehydrogenase. gdhB.

CAA09478.1 AJ011096 Asparagus officinalis
glutamate dehydrogenase. gdhb.

CAA69601.2 Y08293 Nicotiana plumbaginifolia
NADH glutamate dehydrogenase. GDH B.

AAB39508.1 U48695 Lycopersicon esculentum
glutamate dehydrogenase. legdh1.

CAA09456.1 AJ011006 *Asparagus officinalis*
NADH glutamate dehydrogenase. *gdhA*.

CAA41635.1 X58831 *Chlorella sorokiniana*
glutamate dehydrogenase (NADP+). *gdhANC*. There are other coding exons before the first exon given for this gene.

CAA41636.1 X58832 *Chlorella sorokiniana*
glutamate dehydrogenase (NADP+). *gdhANC*.

SEQ ID NO: 412

CAA65456.2 X96681 *Oryza sativa*
transcription factor. DNA-binding protein. *Oshox1*. homeodomain leucine zipper gene.

AAK00416.1 AC069324 *Oryza sativa*
Putative DNA-binding protein. OSJNBa0071K19.2.

BAA05622.1 D26573 *Daucus carota*
transcriptional regulator. DNA-binding protein. homeodomain at nt 585-764; leucine zipper at nt 765-851.

BAA05625.1 D26576 *Daucus carota*
transcriptional regulator. DNA-binding protein. homeodomain at nt 300-479; leucine zipper at nt 480-587.

BAA21017.1 D26578 *Daucus carota*
transcriptional regulator. DNA-binding protein. homeodomain at nt 761-940; leucine zipper at nt 941-1048.

BAA05624.1 D26575 *Daucus carota*
transcriptional regulator. DNA-binding protein. homeodomain at nt 520-699; leucine zipper at nt 700-805.

BAA05623.1 D26574 *Daucus carota*
transcriptional regulator. DNA-binding protein. homeodomain at nt 498-677; leucine zipper at nt 678-785.

SEQ ID NO: 414

BAA95814.1 AP002069 *Oryza sativa*
ESTs AU082579(S2069), D40238(S2069) correspond to a region of the predicted gene.
Similar to *Arabidopsis thaliana* vesicle-associated membrane protein 7C; synaptobrevin 7C.
(AF025332).

SEQ ID NO: 415

CAA45025.1 X63431 *Rauvolfia mannii*
strictosidine synthase. *str1*.

CAA68725.1 Y00756 *Rauvolfia serpentina*
strictosidine synthase.

CAA44208.1 X62334 *Rauvolfia serpentina*
strictosidine synthase. *str1*.

CAA37671.1 X53602 *Catharanthus roseus*
strictosidine synthase precursor.

CAA71255.1 Y10182 *Catharanthus roseus*
strictosidine synthase. *str1*.

CAA43936.1 X61932 Catharanthus roseus
strictosidine synthase. sss.

AAF75751.1 AF261141 Lycopersicon esculentum
putative strictosidine synthase.

CAB53484.1 AJ245900 Oryza sativa

CAA303711.1 protein. q3037.11. Similar to strictosidine synthase 3 precursor.

SEQ ID NO: 418

AAG22607.1 AF258810 Lycopersicon esculentum
aldehyde oxidase. AO3. molybdenum cofactor-binding enzyme.

AAG22606.1 AF258809 Lycopersicon esculentum
aldehyde oxidase. AO2. molybdenum cofactor-binding enzyme.

AAG22605.1 AF258808 Lycopersicon esculentum
aldehyde oxidase. AO1. molybdenum cofactor-binding enzyme.

BAA23227.1 D88452 Zea mays
aldehyde oxidase-2. zmAO-2. putative.

BAA23226.1 D88451 Zea mays
aldehyde oxidase. zmAO-1.

AAB41742.1 U82559 Lycopersicon esculentum
aldehyde oxidase 1 homolog. TAO1. has sequence properties of the molybdenum cofactor
containing the hydroxylase genes aldehyde oxidase and xanthine dehydrogenase; belongs to a
multigene family.

AAG22608.1 AF259793 Lycopersicon esculentum
aldehyde oxidase. AO1. molybdenum cofactor-binding enzyme.

AAB41741.1 U82558 Lycopersicon esculentum
aldehyde oxidase 1 homolog. TAO1. has sequence properties of the molybdenum cofactor
containing the hydroxylase genes aldehyde oxidase and xanthine dehydrogenase; belongs to a
multigene family.

SEQ ID NO: 421

BAA13635.1 D88530 Spinacia oleracea
serine acetyltransferase.

BAA13634.1 D88529 Spinacia oleracea
serine acetyltransferase.

BAA93050.1 AB040502 Allium tuberosum
serine acetyltransferase. ASAT5.

BAA08479.1 D49535 Citrullus lanatus
serine acetyltransferase.

BAA12843.1 D85624 Citrullus lanatus
serine acetyltransferase. Sat.

BAA21827.1 AB006530 Citrullus lanatus
serine acetyltransferase. Sat.

AAF19000.1 AF212156 Allium cepa
serine acetyltransferase.

SEQ ID NO: 422

BAA05079.1	D26086	Petunia x hybrida	zinc-finger protein.
CAB77055.1	Y18788	Medicago sativa	putative TFIIIA (or kruppel)-like zinc finger protein.
AAD26942.1	AF119050	Datisca glomerata	zinc-finger protein 1. zfp1. DgZFP1.
AAB39638.1	U68763	Glycine max	putative transcription factor. SCOF-1. scof-1. zinc-finger protein.
AAC06243.1	AF053077	Nicotiana tabacum	transcription factor. osmotic stress-induced zinc-finger protein. zfp.
BAA05077.1	D26084	Petunia x hybrida	zinc-finger DNA binding protein.
BAA05076.1	D26083	Petunia x hybrida	zinc-finger DNA binding protein.
BAA05078.1	D26085	Petunia x hybrida	zinc-finger DNA binding protein.
AAK01713.1	AF332876	Oryza sativa	zinc finger transcription factor ZF1.
AAB53260.1	U76554	Brassica rapa	transcription factor. zinc-finger protein-1. BR42.
AAB53261.1	U76555	Brassica rapa	zinc-finger protein BcZFP1. BcZFP1(3-2z).
BAA96070.1	AB035132	Petunia x hybrida	C2H2 zinc-finger protein ZPT2-10. PEThy;ZPT2-10.
BAA21919.1	AB006597	Petunia x hybrida	ZPT2-10. C2H2 zinc finger protein, 2 finger.
BAA96071.1	AB035133	Petunia x hybrida	C2H2 zinc-finger protein ZPT3-3. ZPT3-3.
BAA21927.1	AB006605	Petunia x hybrida	ZPT3-3. C2H2 zinc finger protein, 3 finger.
BAA19112.1	AB000453	Petunia x hybrida	PEThy;ZPT3-1. Cys(2) His(2) zinc finger protein, 3 fingers.
BAA21928.1	AB006606	Petunia x hybrida	ZPT4-4. C2H2 zinc finger protein, 4 finger.
BAA21922.1	AB006600	Petunia x hybrida	ZPT2-13. C2H2 zinc finger protein, 2finger.
BAA19114.1	AB000455	Petunia x hybrida	PEThy;ZPT4-1. Cys(2) His(2) zinc finger protein, 4 fingers.
BAA21920.1	AB006598	Petunia x hybrida	ZPT2-11. C2H2 zinc finger protein, 2finger.
BAA21921.1	AB006599	Petunia x hybrida	ZPT2-12. C2H2 zinc finger protein, 2 finger.

BAA19110.1 AB000451 *Petunia x hybrida*
 PETHy;ZPT2-5. Cys(2) His(2) zinc finger protein, 2 fingers.

BAA21926.1 AB006604 *Petunia x hybrida*
 ZPT2-9. C2H2 zinc finger protein, 2 finger.

BAA21925.1 AB006603 *Petunia x hybrida*
 ZPT2-8. C2H2 zinc finger protein, 2 finger.

CAA60828.1 X87374 *Pisum sativum*
 putative zinc finger protein.

BAA19111.1 AB000452 *Petunia x hybrida*
 PETHy;ZPT2-6. Cys(2) His(2) zinc finger protein, 2 fingers.

BAA21923.1 AB006601 *Petunia x hybrida*
 ZPT2-14. C2H2 zinc finger protein, 2 finger.

BAA21924.1 AB006602 *Petunia x hybrida*
 ZPT2-7. C2H2 zinc finger protein, 2finger.

BAA19113.1 AB000454 *Petunia x hybrida*
 PETHy;ZPT3-2. Cys(2) His(2) zinc finger protein, 3 fingers.

BAA19926.1 AB000456 *Petunia x hybrida*
 PETHy; ZPT4-2. C2H2 zinc finger protein, 4 finger.

SEQ ID NO: 423

AAC49815.1 U87257 *Daucus carota*
 4-hydroxyphenylpyruvate dioxygenase.

CAA04245.1 AJ000693 *Hordeum vulgare*
 4-hydroxyphenylpyruvate dioxygenase.

SEQ ID NO: 424

AAC72193.1 AF069909 *Zea mays*
 pyruvate dehydrogenase E1 beta subunit isoform 2.

AAC72192.1 AF069908 *Zea mays*
 pyruvate dehydrogenase E1 beta subunit isoform 1.

AAC72194.1 AF069910 *Zea mays*
 pyruvate dehydrogenase E1 beta subunit isoform 3.

AAB01223.1 U56697 *Pisum sativum*
 pyruvate dehydrogenase E1beta.

AAC32149.1 AF051249 *Picea mariana*
 pyruvate dehydrogenase E1 beta subunit. Sb68.

AAF43837.1 AF166114 *Chloroplast Mesostigma viride*
 beta subunit of pyruvate dehydrogenase E1 component. odpB.

AAD22077.1 AF124755 *Pinus banksiana*
 pyruvate dehydrogenase E1 beta subunit. Sb68.

CAA75778.1 Y15782 *Capsicum annuum*
 transketolase 2.

AAB88295.1 AF024512 *Oryza sativa*
 CLA1 transketolase-like protein. CLA1. similar to Arabidopsis CLA1 product; required for chloroplast development.

SEQ ID NO: 426

AAB53764.1 U96713 Brassica rapa
aminoalcoholphosphotransferase. AAPT1.

AAD56040.1 AF183933 Brassica rapa
aminoalcoholphosphotransferase. AAPT3.

AAC79507.1 U96439 Pimpinella brachycarpa
aminoalcoholphosphotransferase. AAPTase.

AAA67719.1 U12735 Glycine max
CDP-choline:diacylglycerol cholinephosphotransferase activity and possibly CDP-ethanolamine: diacylglycerol ethanolaminephosphotransferase activity.
aminoalcoholphosphotransferase. AAPT1.

SEQ ID NO: 427

CAA56313.1 X79992 Avena sativa
putative pp70 ribosomal protein S6 kinase. Aspk11.

CAB89082.1 AJ277534 Asparagus officinalis
S6 ribosomal protein kinase. pk1. putative.

AAK18843.1 AC082645 Oryza sativa
putative protein kinase. OSJNBb0033N16.3.

AAC05084.1 AF033097 Avena sativa
NPH1-2. NPH1-2. putative serine/threonine protein kinase.

AAC05083.1 AF033096 Avena sativa
NPH1-1. NPH1-1. putative serine/threonine protein kinase.

AAK13156.1 AC078829 Oryza sativa
putative protein kinase. OSJNBa0026O12.14.

AAB88817.1 AF033263 Zea mays
signal transduction for phototropism. nonphototropic hypocotyl 1. nph1. NPH1; putative serine/threonine kinase; similar to oat NPH1 proteins.

CAB82852.1 Z30329 Mesembryanthemum crystallinum
protein kinase MK6.

BAB18104.1 AB042714 Chlamydomonas reinhardtii
cyclic nucleotide dependent protein kinase. CL-PK1.

BAB18105.1 AB042715 Chlamydomonas reinhardtii
cyclic nucleotide dependent protein kinase II. CL-PK2.

BAA83689.1 AB011968 Oryza sativa
OsPK7. OsPK7. protein kinase.

AAD31900.1 AF145482 Mesembryanthemum crystallinum
putative serine/threonine protein kinase.

BAA92970.1 AP001551 Oryza sativa
Similar to Arabidopsis thaliana chromosome 4 BAC clone F28A21 ; putative protein kinase. (AL035526).

BAA92972.1	AP001551	Oryza sativa	ESTs AU056183(S20356),AU056881(S20950) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 4 BAC clone F6I18 ; putative protein kinase. (AL022198).
BAA83688.1	AB011967	Oryza sativa	OsPK4. OsPK4. protein kinase.
AAF22219.1	AF141378	Zea mays	protein kinase PK4. ZmPK4.
CAA73067.1	Y12464	Sorghum bicolor	serine/threonine kinase. SNFL1.
BAA96628.1	AP002482	Oryza sativa	ESTs D41739(S4522),AU055999(S20214), AU057588(S21592) correspond to a region of the predicted gene. Similar to Sorghum bicolor serine/threonine kinase (Y12465).
CAA89202.1	Z49233	Chlamydomonas eugametos	calcium-stimulated protein kinase.
CAA73068.1	Y12465	Sorghum bicolor	serine/threonine kinase. SNFL2.
BAA34675.1	AB011670	Triticum aestivum	wpk4 protein kinase. wpk4.
CAA74646.1	Y14274	Sorghum bicolor	putative serine/threonine protein kinase. SNFL3.
AAF06970.1	AF162662	Kalanchoe fedtschenkoi	phosphoenolpyruvate carboxylase kinase. calcium-independent protein kinase.
AAF06969.1	AF162661	Kalanchoe fedtschenkoi	phosphoenolpyruvate carboxylase kinase. calcium-independent protein kinase.
CAA39936.1	X56599	Daucus carota	calcium- dependent protein kinase. DcPK431.
BAA99439.1	AP002743	Oryza sativa	putative protein kinase. P0710E05.26. contains ESTs C22394(C30013),C22393(C30013).
BAA90814.1	AP001168	Oryza sativa	ESTs AU030197(E50746),AU030196(E50746) correspond to a region of the predicted gene.; Similar to calcium-dependent calmodulin-independent protein kinase CDPK (U90262).
BAB12687.1	AP002746	Oryza sativa	putative protein kinase. P0671B11.2. contains ESTs C22394(C30013),C22393(C30013).
AAB62693.1	AF004947	Oryza sativa	protein kinase.
CAA71142.1	Y10036	Cucumis sativus	SNF1-related protein kinase.
BAA05649.1	D26602	Nicotiana tabacum	protein kinase.
AAC25423.1	AF072908	Nicotiana tabacum	calcium-dependent protein kinase. CDPK1.

AAF19403.1	AF203481	<i>Lycopersicon esculentum</i> phosphoenolpyruvate carboxylase kinase. protein kinase; member of Ca ²⁺ /CaM kinase family; lacks the autoinhibitory region and EF hands.
AAF21062.1	AF216527	<i>Dunaliella tertiolecta</i> calcium-dependent protein kinase. CPK1; CDPK.
AAF19402.1	AF203480	<i>Lycopersicon esculentum</i> phosphoenolpyruvate carboxylase kinase. protein kinase; member of Ca ²⁺ /CaM kinase family; lacks the autoinhibitory region and EF hands.
CAA65244.1	X95997	<i>Solanum tuberosum</i> SNF1-related protein kinase. PKIN1.
CAA57898.1	X82548	<i>Hordeum vulgare</i> SNF1-related protein kinase. BKIN2.
BAA13608.1	D88399	<i>Oryza sativa</i> serine-threonine kinase. endosperm kinase. REK.
CAA08995.1	AJ010091	<i>Brassica napus</i> MAP3K alpha 1 protein kinase. MAP3K alpha 1.
AAF19401.1	AF203479	<i>Glycine max</i> phosphoenolpyruvate carboxylase kinase. protein kinase; member of Ca ²⁺ /CaM kinase family; lacks the autoinhibitory region and EF hands.
BAA05648.1	D26601	<i>Nicotiana tabacum</i> protein kinase.
AAC69450.1	AF032465	<i>Nicotiana tabacum</i> putative serine/threonine protein kinase. WAPK.
AAD23582.1	AF128443	<i>Glycine max</i> probably involved in plant stress responses possibly regulates gene expression. SNF-1-like serine/threonine protein kinase. expressed in nodules, roots and leaves.
AAD00239.1	U73938	<i>Nicotiana tabacum</i> protein kinase. PK11-C1. PK11-C1. induced at the transcriptional level by the abscisic acid plant hormone; similar to serine/threonine protein kinase.
AAG60195.1	AC084763	<i>Oryza sativa</i> protein kinase REK. OSJNBa0027P10.6.
SEQ ID NO: 428		
CAC17753.1	AJ294543	<i>Dendrobium 'Sonia'</i> metabolic enzyme of cytokinins. cytokinin oxidase. cko1.
CAC17752.1	AJ294542	<i>Dendrobium 'Sonia'</i> metabolic enzyme of cytokinins. cytokinin oxidase. cko1.
CAA77151.1	Y18377	<i>Zea mays</i> cytokinin oxidase. cko.
AAC27500.1	AF044603	<i>Zea mays</i> cytokinin oxidase. cko1.
BAB07927.1	AP002836	<i>Oryza sativa</i> putative cytokinin oxidase. P0512G09.9.

BAB03420.1 AP002816 *Oryza sativa*
Similar to *Zea mays* mRNA for cytokinin oxidase. (Y18377).

SEQ ID NO: 429

BAA21922.1 AB006600 *Petunia x hybrida*
ZPT2-13. C2H2 zinc finger protein, 2finger.

BAA21923.1 AB006601 *Petunia x hybrida*
ZPT2-14. C2H2 zinc finger protein, 2 finger.

BAA21921.1 AB006599 *Petunia x hybrida*
ZPT2-12. C2H2 zinc finger protein, 2 finger.

BAA19110.1 AB000451 *Petunia x hybrida*
PETHy;ZPT2-5. Cys(2) His(2) zinc finger protein, 2 fingers.

BAA21925.1 AB006603 *Petunia x hybrida*
ZPT2-8. C2H2 zinc finger protein, 2 finger.

BAA21926.1 AB006604 *Petunia x hybrida*
ZPT2-9. C2H2 zinc finger protein, 2 finger.

BAA21924.1 AB006602 *Petunia x hybrida*
ZPT2-7. C2H2 zinc finger protein, 2finger.

BAA19111.1 AB000452 *Petunia x hybrida*
PETHy;ZPT2-6. Cys(2) His(2) zinc finger protein, 2 fingers.

BAA05077.1 D26084 *Petunia x hybrida*
zinc-finger DNA binding protein.

AAD26942.1 AF119050 *Datisca glomerata*
zinc-finger protein 1. zfp1. DgZFP1.

BAA05076.1 D26083 *Petunia x hybrida*
zinc-finger DNA binding protein.

CAB77055.1 Y18788 *Medicago sativa*
putative TFIIIA (or kruppel)-like zinc finger protein.

AAC06243.1 AF053077 *Nicotiana tabacum*
transcription factor. osmotic stress-induced zinc-finger protein. zfp.

BAA21927.1 AB006605 *Petunia x hybrida*
ZPT3-3. C2H2 zinc finger protein, 3 finger.

BAA96071.1 AB035133 *Petunia x hybrida*
C2H2 zinc-finger protein ZPT3-3. ZPT3-3.

BAA21920.1 AB006598 *Petunia x hybrida*
ZPT2-11. C2H2 zinc finger protein, 2finger.

AAB53261.1 U76555 *Brassica rapa*
zinc-finger protein BcZFP1. BcZFP1(3-2z).

AAB53260.1 U76554 *Brassica rapa*
transcription factor. zinc-finger protein-1. BR42.

CAA60828.1 X87374 *Pisum sativum*
putative zinc finger protein.

AAB39638.1 U68763 Glycine max
putative transcription factor. SCOF-1. scof-1. zinc-finger protein.

AAK01713.1 AF332876 Oryza sativa
zinc finger transcription factor ZF1.

BAA05079.1 D26086 Petunia x hybrida
zinc-finger protein.

BAA96070.1 AB035132 Petunia x hybrida
C2H2 zinc-finger protein ZPT2-10. PETHy;ZPT2-10.

BAA21919.1 AB006597 Petunia x hybrida
ZPT2-10. C2H2 zinc finger protein, 2 finger.

BAA05078.1 D26085 Petunia x hybrida
zinc-finger DNA binding protein.

BAA19112.1 AB000453 Petunia x hybrida
PETHy;ZPT3-1. Cys(2) His(2) zinc finger protein, 3 fingers.

BAA19114.1 AB000455 Petunia x hybrida
PETHy;ZPT4-1. Cys(2) His(2) zinc finger protein, 4 fingers.

BAA21928.1 AB006606 Petunia x hybrida
ZPT4-4. C2H2 zinc finger protein, 4 finger.

BAA19926.1 AB000456 Petunia x hybrida
PETHy; ZPT4-2. C2H2 zinc finger protein, 4 finger.

SEQ ID NO: 432

AAC05084.1 AF033097 Avena sativa
NPH1-2. NPH1-2. putative serine/threonine protein kinase.

AAC05083.1 AF033096 Avena sativa
NPH1-1. NPH1-1. putative serine/threonine protein kinase.

CAA82993.1 Z30332 Spinacia oleracea
protein kinase.

AAB88817.1 AF033263 Zea mays
signal transduction for phototropism. nonphototropic hypocotyl 1. nph1. NPH1; putative serine/threonine kinase; similar to oat NPH1 proteins.

CAB65325.1 AJ252142 Oryza sativa
putative blue light receptor phototropin. non-phototropic hypocotyl NPH1. nph1.

CAA82994.1 Z30333 Mesembryanthemum crystallinum
protein kinase.

BAA36192.1 AB012082 Adiantum capillus-veneris
PHY3. PHY3. Ser/Thr protein kinase; chimeric structure of red/far-red light photoreceptive region (phytochrome) and putative blue light photoreceptor in phototropism of hypocotyl (NPH1).

SEQ ID NO: 446

AAB72047.1 AF006489 Gossypium hirsutum
adenine nucleotide translocator 1. CANT1.

CAA05979.1 AJ003197 Lupinus albus
transfer of ATP from mitochondria to cytosol. adenine nucleotide translocator. ant1.

CAA44054.1	X62123	Solanum tuberosum	ADP /ATP translocator. ant. product has dimeric subunit structure.
AAB49700.1	U89839	Lycopersicon esculentum	ADP/ATP translocator.
CAA40782.1	X57557	Solanum tuberosum	adenine nucleotide translocator. AAC.
BAA02161.1	D12637	Oryza sativa	ATP/ADP translocator.
CAA41812.1	X59086	Zea mays	adenine nucleotide translocator. MANT2.
CAA40781.1	X57556	Zea mays	adenine nucleotide translocator. MANT1.
CAA33743.1	X15712	Zea mays	adenine nucleotide translocator.
CAA33742.1	X15711	Zea mays	adenine nucleotide translocator.
CAA65119.1	X95863	Triticum turgidum	adenine nucleotide translocator.
CAA26600.1	X02842	Zea mays	put. ATP/ADP translocator.
CAA65120.1	X95864	Triticum turgidum	adenine nucleotide translocator.
CAA46311.1	X65194	Chlamydomonas reinhardtii	mitochondrial ADP/ATP translocator protein. CRANT.
AAA33027.1	M76669	Chlorella kessleri	ATP/ADP translocator. AAT.
AAB72048.1	AF006490	Gossypium hirsutum	adenine nucleotide translocator 2. CANT2.
BAA08104.1	D45074	Panicum miliaceum	2-oxoglutarate/malate translocator. mitochondrial 2-oxoglutarate/malate translocator.
BAA08103.1	D45073	Panicum miliaceum	2-oxoglutarate/malate translocator. mitochondrial 2-oxoglutarate/malate translocator.
BAA08105.1	D45075	Panicum miliaceum	2-oxoglutarate/malate translocator. mitochondrial 2-oxoglutarate/malate translocator.
SEQ ID NO: 447			
BAB16317.1	AB049589	Avicennia marina	secretory peroxidase. PER.
AAC83463.1	AF039027	Glycine max	H2O2 oxidoreductase. cationic peroxidase 2. Prx2. class III plant peroxidase.
AAD37374.1	AF145348	Glycine max	peroxidase. Prx2b.

CAB71128.2	AJ271660	Cicer arietinum	cationic peroxidase.
AAD33072.1	AF149251	Nicotiana tabacum	secretory peroxidase. PER.
AAA99868.1	L08199	Gossypium hirsutum	peroxidase. putative.
BAA94962.1	AB042103	Asparagus officinalis	peroxidase. AspPOX1.
AAF63027.1	AF244924	Spinacia oleracea	hydrogen peroxide catabolism. peroxidase prx15 precursor. type III peroxidase.
AAF63026.1	AF244923	Spinacia oleracea	hydrogen peroxide catabolism. peroxidase prx14 precursor. type III peroxidase.
BAA92500.1	AP001383	Oryza sativa	ESTs D39300(R3292),AU030751(E60187) correspond to a region of the predicted gene. Similar to peroxidase ATP6a. (X98774).
AAF63025.1	AF244922	Spinacia oleracea	hydrogen peroxide catabolism. peroxidase prx13 precursor. type III peroxidase.
AAG46133.1	AC082644	Oryza sativa	putative peroxidase. OSJNBa0013M12.15.
AAA32973.1	M73234	Hordeum vulgare	peroxidase BP 1. Prx5.
CAA71493.1	Y10467	Spinacia oleracea	peroxidase. prxr6.
AAG46122.1	AC082644	Oryza sativa	putative peroxidase. OSJNBa0013M12.2.
AAG46141.1	AC082644	Oryza sativa	putative peroxidase. OSJNBa0013M12.11.
BAA77387.1	AB024437	Scutellaria baicalensis	peroxidase 1.
AAG46142.1	AC082644	Oryza sativa	putative peroxidase. OSJNBa0013M12.9.
AAB02926.1	U59284	Linum usitatissimum	peroxidase. FLXPER3.
CAA50597.1	X71593	Lycopersicon esculentum	peroxidase. CEVI-1.
BAA82306.1	AB027752	Nicotiana tabacum	peroxidase.
CAB67121.1	Y19023	Lycopersicon esculentum	peroxidase. cevi-1.
AAG46125.1	AC082644	Oryza sativa	putative peroxidase. OSJNBa0013M12.17.

BAA92422.1	AP001366	Oryza sativa	ESTs AU081576(R0541),AU032412(R4029) correspond to a region of the predicted gene. Similar to A.thaliana mRNA for peroxidase ATP18a. (X98804).
BAA92497.1	AP001383	Oryza sativa	ESTs AU081576(R0541),AU032412(R4029) correspond to a region of the predicted gene. Similar to peroxidase ATP18a. (X98804).
CAA59487.1	X85230	Triticum aestivum	peroxidase. pox4.
AAA98491.1	L36981	Petroselinum crispum	anionic peroxidase.
CAA71492.1	Y10466	Spinacia oleracea	peroxidase. prxr5.
BAA96643.1	AP002482	Oryza sativa	Similar to Arabidopsis thaliana peroxidase ATP19a (X98805).
BAB12025.1	AP002820	Oryza sativa	putative peroxidase. P0702D12.1.
AAB02554.1	L37790	Stylosanthes humilis	cationic peroxidase.
AAF63024.1	AF244921	Spinacia oleracea	hydrogen peroxide catabolism. peroxidase prx12 precursor. type III peroxidase.
AAC84140.1	AF101427	Cichorium intybus	peroxidase.
AAA65637.1	L13654	Lycopersicon esculentum	peroxidase. TPX1.
AAC98519.1	AF007211	Glycine max	peroxidase precursor. GMIPER1. pathogen-induced.
BAA14143.1	D90115	Armoracia rusticana	peroxidase isozyme.
CAA62226.1	X90693	Medicago sativa	peroxidase1B. prx1B.
AAD37430.1	AF149280	Phaseolus vulgaris	peroxidase 5 precursor. FBP5. secretory peroxidase.
CAA62615.1	X91232	Mercurialis annua	PRX. peroxidase.
AAG46130.1	AC082644	Oryza sativa	putative peroxidase. OSJNBa0013M12.18.
CAC21392.1	AJ401275	Zea mays	peroxidase. pox2.
BAA07241.1	D38051	Populus kitakamiensis	peroxidase. prxA4a.
BAB39277.1	AP002971	Oryza sativa	putative peroxidase. P0537A05.6. contains ESTs C23550(C52903),C97179(C52903).

CAB65334.1 AJ250121 *Picea abies*
peroxidase. SPI2 protein. spi2.

CAA62597.1 X91172 *Raphanus sativus*
korean-radish isoperoxidase. prxk1.

AAC49820.1 AF014469 *Oryza sativa*
peroxidase. POX5.1. wound inducible.

CAA71496.1 Y10470 *Spinacia oleracea*
peroxidase. prxr9.

BAA01950.1 D11337 *Vigna angularis*
peroxidase.

CAA71491.1 Y10465 *Spinacia oleracea*
peroxidase. prxr4.

BAA03911.1 D16442 *Oryza sativa*
peroxidase.

SEQ ID NO: 449

CAA56325.1 X80023 *Triticum turgidum*
ATP/ADP carrier protein.

CAC27140.1 AJ132535 *Picea abies*
ADP, ATP carrier protein precursor.

BAA92520.1 AP001383 *Oryza sativa*
ESTs AU068633(C30614),AU068634(C30614) correspond to a region of the predicted gene.
Similar to *Bos taurus* mitochondrial solute carrier protein. (AF049236).

BAB16462.1 AP002483 *Oryza sativa*
putative peroxisomal Ca-dependent solute carrier protein. P0019D06.21.

BAB40117.1 AP003311 *Oryza sativa*
putative peroxisomal Ca-dependent solute carrier protein. P0024G09.9.

AAB71744.1 U75346 *Chlamydomonas reinhardtii*
envelope protein. LIP-36G2. low CO₂ inducible carrier protein LIP-36 with a molecular
weight of 36 kDa.

AAB71743.1 U75345 *Chlamydomonas reinhardtii*
envelope protein. LIP-36G1. low CO₂ inducible carrier protein LIP-36 with a molecular
weight of 36 kDa.

AAG48999.1 AY013246 *Hordeum vulgare*
putative mitochondrial carrier protein. 635P2.1.

CAC12820.1 AJ299250 *Nicotiana tabacum*
mitochondrial 2-oxoglutarate/malate carrier protein. momc1.

CAA07568.1 AJ007580 *Ribes nigrum*
Mitochondrial carrier protein. prib7.

AAG45489.1 AY013245 *Oryza sativa*
36I5.1. putative mitochondrial carrier protein.

SEQ ID NO: 451

AAB53099.1 U68217 *Brassica napus*
iron binding protein. ferritin. LSC30.

AAA33959.1	M64337	Glycine max ferritin light chain. ferritin.
AAA34016.1	M72894	Glycine max ferritin light chain. SOF-H2.
CAA65771.1	X97059	Medicago sativa iron storage. ferritin. FER. abscisic acid regulated.
AAB18928.1	U31648	Glycine max iron storage protein. ferritin.
AAC06026.1	AF052057	Vigna unguiculata iron storage and mobilization in plants. ferritin subunit cowpea3 precursor.
AAC06027.1	AF052058	Vigna unguiculata iron storage and mobilization in plants. ferritin subunit cowpea2 precursor.
CAA41213.1	X58274	Phaseolus vulgaris ferritin. pfe.
AAD50644.1	AF133814	Solanum tuberosum ferritin 1. F1.
CAA51786.1	X73369	Pisum sativum ferritin.
CAA45763.1	X64417	Pisum sativum ferritin-precursor.
CAA43663.1	X61391	Zea mays ferritin.
CAA58146.1	X83076	Zea mays ferritin. Fer1.
CAA58147.1	X83077	Zea mays ferritin. Fer2.
CAA43664.1	X61392	Zea mays ferritin.
AAA33958.1	M58336	Glycine max ferritin light chain. SOF-5L.
CAB42587.1	AJ238628	Chlorella protothecoides putative ferritin. dee188.
BAB17852.1	AB042612	Nicotiana tabacum ferritin 1. tob-fer-1. putative.
AAC15241.1	AF028072	Pinus taeda ferritin.
CAA47982.1	X67754	Vigna unguiculata ferritin 1. pfe1.
CAA47984.1	X67756	Vigna unguiculata ferritin 5. pfe5.
CAA47983.1	X67755	Vigna unguiculata ferritin 2. pfe2.

AAC12282.1 AF052511 Glycine max
iron storage and mobilization. ferritin 2. soybean 2; cowpea 2 homolog.

AAC12281.1 AF052513 Glycine max
iron storage and mobilization. ferritin 1. soybean 1; cowpea 1 homolog.

SEQ ID NO: 452

CAB56619.1 AJ244024 Nicotiana tabacum
putative role in cell plate formation. phragmoplastin. phragmoplastin. dynamin-like protein.

SEQ ID NO: 454

CAA55039.1 X78203 Hyoscyamus muticus
glutathione transferase.

AAB65163.1 AF002692 Solanum commersonii
glutathione S-transferase, class-phi. GST1. low temperature induced.

BAA01394.1 D10524 Nicotiana tabacum
glutathione S-transferase. parB.

CAA96431.1 Z71749 Nicotiana plumbaginifolia
glutathione S-transferase.

AAA33931.1 M84969 Silene vulgaris
glutathione-S-transferase.

AAA33930.1 M84968 Silene vulgaris
glutathione-S-transferase.

AAF65767.1 AF242309 Euphorbia esula
glutathione S-transferase. putative auxin-binding GST.

AAF61392.1 AF133894 Persea americana
glutathione S-transferase. GTH.

CAB38119.1 AJ010296 Zea mays
Glutathione transferase III(b). gst3b.

CAB38118.1 AJ010295 Zea mays
Glutathione transferase III(a). gst3a.

BAB39935.1 AP002914 Oryza sativa
putative glutathione S-transferase. P0493G01.17.

AAG34811.1 AF243376 Glycine max
glutathione S-transferase GST 21.

BAB39939.1 AP002914 Oryza sativa
putative glutathione S-transferase. P0493G01.21.

AAG34812.1 AF243377 Glycine max
glutathione S-transferase GST 22.

AAG34814.1 AF243379 Glycine max
glutathione S-transferase GST 24.

CAA09190.1 AJ010451 Alopecurus myosuroides
glutathione transferase. GST2a.

AAG32476.1 AF309383 Oryza sativa subsp. japonica
putative glutathione S-transferase OsGSTF4.

BAB39929.1	AP002914	Oryza sativa	putative glutathione transferase. P0493G01.7.
CAA09193.1	AJ010454	Alopecurus myosuroides	glutathione transferase. GST2d.
BAB39941.1	AP002914	Oryza sativa	putative glutathione S-transferase. P0493G01.23.
CAA09191.1	AJ010452	Alopecurus myosuroides	glutathione transferase. GST2b.
CAA09192.1	AJ010453	Alopecurus myosuroides	glutathione transferase. GST2c.
AAD56395.1	AF184059	Triticum aestivum	glutathione S-transferase. GST1.
CAA39487.1	X56012	Triticum aestivum	glutathione transferase. gstA1.
AAG32477.1	AF309384	Oryza sativa subsp. japonica	putative glutathione S-transferase OsGSTF3.
CAA68993.1	Y07721	Petunia x hybrida	conjugates glutathione to anthocyanin to facilitate transport to the vacuole. glutathione S-transferase. an9 locus.
AAA33470.1	M16901	Zea mays	glutathione S-transferase I.
AAA33469.1	M16902	Zea mays	glutathione S-transferase I.
AAA20585.1	U12679	Zea mays	glutathione S-transferase IV. GSTIV.
CAA56047.1	X79515	Zea mays	glutathione transferase. GST27.
CAB66333.1	AJ279691	Betula pendula	glutathione-S-transferase. gst.
BAB39927.1	AP002914	Oryza sativa	putative glutathione S-transferase. P0493G01.1. contains ESTs AU031696(R0596),C97559(C60386),C28218(C60386), D28287(R0596).
AAC64007.1	AF062403	Oryza sativa	glutathione S-transferase II.
CAA39480.1	X56004	Triticum aestivum	glutathione transferase. gstA2.
AAG32475.1	AF309382	Oryza sativa subsp. japonica	putative glutathione S-transferase OsGSTF5.
AAG34823.1	AF244680	Zea mays	glutathione S-transferase GST 15.
BAB39940.1	AP002914	Oryza sativa	putative glutathione S-transferase. P0493G01.22.

AAG34818.1 AF244675 Zea mays
glutathione S-transferase GST 10.

AAG34820.1 AF244677 Zea mays
glutathione S-transferase GST 11.

AAG34817.1 AF244674 Zea mays
glutathione S-transferase GST 9.

AAG34821.1 AF244678 Zea mays
glutathione S-transferase GST 13.

CAA05354.1 AJ002380 Oryza sativa
glutathione S-transferase. Rgst I.

AAG34816.1 AF244673 Zea mays
glutathione S-transferase GST 8.

AAG34822.1 AF244679 Zea mays
glutathione S-transferase GST 14.

CAA05355.1 AJ002381 Oryza sativa
glutathione S-transferase. Rgst II.

SEQ ID NO: 458

AAD45623.1 AF084185 Brassica napus
dehydration responsive element binding protein. DNA binding protein; DRE binding protein.

BAA90812.1 AP001168 Oryza sativa
Similar to mRNA for DREB1A (AB007787).

AAK01089.1 AF298231 Hordeum vulgare
CBF3-like protein BCBF3. BCBF3. AP2 domain protein; DRE binding factor.

AAG59618.1 AF239616 Hordeum vulgare
CRT/DRE-binding factor. CBF.

AAK01088.1 AF298230 Hordeum vulgare
CBF1-like protein BCBF1. BCBF1. AP2 domain protein; putative DRE binding factor.

AAG59619.1 AF243384 Oryza sativa
CRT/DRE binding factor. CBF. DREB.

AAC29516.1 U77655 Solanum tuberosum
DNA binding protein homolog. STWAAEIRD.

BAA76734.1 AB024575 Nicotiana tabacum
ethylene responsive element binding factor.

CAB93939.1 AJ238739 Catharanthus roseus
putative transcription factor. AP2-domain DNA-binding protein. orcal.

BAB03248.1 AB037183 Oryza sativa
ERF protein transcriptional repressor. ethylene responsive element binding factor3. osERF3.

BAA97123.1 AB016265 Nicotiana glauca
ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf3.

BAA97124.1 AB016266 Nicotiana glauca
ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf4.

AAC50047.1	U89255	<i>Lycopersicon esculentum</i>	binds the GCC box pathogenesis-related promoter element DNA-binding protein. Pti4.
AAD00708.1	U91857	<i>Stylosanthes hamata</i>	ethylene-responsive element binding protein homolog. similar to EREBP1, -2, -3 and -4 proteins encoded by GenBank Accession Numbers D38123, D38126, D38124, and D38125 respectively.
AAC14323.1	AF058827	<i>Nicotiana tabacum</i>	TSI1. Tsi1. contains putative AP2 DNA-binding domain; similar to Pti6.
AAG60182.1	AC084763	<i>Oryza sativa</i>	putative ethylene-responsive element binding protein. OSJNBa0027P10.12.
AAK31279.1	AC079890	<i>Oryza sativa</i>	putative ethylene-responsive element binding protein. OSJNBb0089A17.16.
AAC49741.1	U89257	<i>Lycopersicon esculentum</i>	DNA-binding protein binds the GCC box pathogenesis-related promoter element. Pti6.
BAA97122.1	AB016264	<i>Nicotiana sylvestris</i>	ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf2.
CAB96900.1	AJ251250	<i>Catharanthus roseus</i>	transcription factor. AP2-domain DNA-binding protein. orca3.
CAB96899.1	AJ251249	<i>Catharanthus roseus</i>	transcription factor. AP2-domain DNA-binding protein. orca3.
BAB21218.1	AP002913	<i>Oryza sativa</i>	putative DNA binding protein RAV2. P0480E02.24.
CAB93940.1	AJ238740	<i>Catharanthus roseus</i>	putative transcription factor. AP2-domain DNA-binding protein. orca2.
BAA87068.1	AB035270	<i>Matricaria chamomilla</i>	ethylene-responsive element binding protein1 homolog. McEREBP1.
AAC49740.1	U89256	<i>Lycopersicon esculentum</i>	binds the GCC box pathogenesis-related promoter element DNA-binding protein. Pti5.
AAB38748.1	U81157	<i>Nicotiana tabacum</i>	S25-XP1 DNA binding protein.
BAB21211.1	AP002913	<i>Oryza sativa</i>	putative DNA binding protein RAV2. P0480E02.17.
BAA78732.1	AB023482	<i>Oryza sativa</i>	Similar to Arabidopsis thaliana mRNA for DREB1B, complete cds.(AB007788).
SEQ ID NO: 460			
AAB67721.1	AF015269	<i>Zea mays</i>	PL transcription factor. Pl. nonfunctional due to retrotransposon insertion.
SEQ ID NO: 461			
AAD50592.1	AF093752	<i>Triticum aestivum</i>	phytochelatase. PCS1.
AAG22095.1	AF308658	<i>Typha latifolia</i>	phytochelatase.

SEQ ID NO: 463

AAG13629.1 AC078840 *Oryza sativa*
putative steroid membrane binding protein. OSJNBb0073N24.4.

AAG13623.1 AC078840 *Oryza sativa*
putative steroid membrane binding protein. OSJNBb0073N24.2.

SEQ ID NO: 464

CAA56313.1 X79992 *Avena sativa*
putative pp70 ribosomal protein S6 kinase. Aspk11.

CAB89082.1 AJ277534 *Asparagus officinalis*
S6 ribosomal protein kinase. pk1. putative.

AAK18843.1 AC082645 *Oryza sativa*
putative protein kinase. OSJNBb0033N16.3.

AAC05083.1 AF033096 *Avena sativa*
NPH1-1. NPH1-1. putative serine/threonine protein kinase.

AAC05084.1 AF033097 *Avena sativa*
NPH1-2. NPH1-2. putative serine/threonine protein kinase.

AAK13156.1 AC078829 *Oryza sativa*
putative protein kinase. OSJNBa0026O12.14.

CAB82852.1 Z30329 *Mesembryanthemum crystallinum*
protein kinase MK6.

AAB88817.1 AF033263 *Zea mays*
signal transduction for phototropism. nonphototropic hypocotyl 1. nph1. NPH1; putative serine/threonine kinase; similar to oat NPH1 proteins.

BAB18105.1 AB042715 *Chlamydomonas reinhardtii*
cyclic nucleotide dependent protein kinase II. CL-PK2.

BAB18104.1 AB042714 *Chlamydomonas reinhardtii*
cyclic nucleotide dependent protein kinase. CL-PK1.

BAA83689.1 AB011968 *Oryza sativa*
OsPK7. OsPK7. protein kinase.

BAA92970.1 AP001551 *Oryza sativa*
Similar to *Arabidopsis thaliana* chromosome 4 BAC clone F28A21 ; putative protein kinase. (AL035526).

AAD31900.1 AF145482 *Mesembryanthemum crystallinum*
putative serine/threonine protein kinase.

BAA92972.1 AP001551 *Oryza sativa*
ESTs AU056183(S20356), AU056881(S20950) correspond to a region of the predicted gene. Similar to *Arabidopsis thaliana* chromosome 4 BAC clone F6I18 ; putative protein kinase. (AL022198).

BAA83688.1 AB011967 *Oryza sativa*
OsPK4. OsPK4. protein kinase.

CAA73067.1 Y12464 *Sorghum bicolor*
serine/threonine kinase. SNFL1.

AAF22219.1	AF141378	Zea mays	protein kinase PK4. ZmPK4.
BAA96628.1	AP002482	Oryza sativa	ESTs D41739(S4522), AU055999(S20214), AU057588(S21592 correspond to a region of the predicted gene. Similar to Sorghum bicolor serine/threonine kinase (Y12465).
CAA89202.1	Z49233	Chlamydomonas eugametos	calcium-stimulated protein kinase.
CAA73068.1	Y12465	Sorghum bicolor	serine/threonine kinase. SNFL2.
BAA34675.1	AB011670	Triticum aestivum	wpk4 protein kinase. wpk4.
BAA99439.1	AP002743	Oryza sativa	putative protein kinase. P0710E05.26. contains ESTs C22394(C30013), C22393(C30013).
CAA74646.1	Y14274	Sorghum bicolor	putative serine/threonine protein kinase. SNFL3.
BAB12687.1	AP002746	Oryza sativa	putative protein kinase. P0671B11.2. contains ESTs C22394(C30013), C22393(C30013).
AAF06969.1	AF162661	Kalanchoe fedtschenkoi	phosphoenolpyruvate carboxylase kinase. calcium-independent protein kinase.
AAF06970.1	AF162662	Kalanchoe fedtschenkoi	phosphoenolpyruvate carboxylase kinase. calcium-independent protein kinase.
BAA90814.1	AP001168	Oryza sativa	ESTs AU030197(E50746), AU030196(E50746) correspond to a region of the predicted gene.; Similar to calcium-dependent calmodulin-independent protein kinase CDPK (U90262).
AAB62693.1	AF004947	Oryza sativa	protein kinase.
AAF21062.1	AF216527	Dunaliella tertiolecta	calcium-dependent protein kinase. CPK1; CDPK.
CAA71142.1	Y10036	Cucumis sativus	SNF1-related protein kinase.
CAA39936.1	X56599	Daucus carota	calcium- dependent protein kinase. DcPK431.
CAA08995.1	AJ010091	Brassica napus	MAP3K alpha 1 protein kinase. MAP3K alpha 1.
BAA05649.1	D26602	Nicotiana tabacum	protein kinase.
AAF19403.1	AF203481	Lycopersicon esculentum	phosphoenolpyruvate carboxylase kinase. protein kinase; member of Ca ²⁺ /CaM kinase family; lacks the autoinhibitory region and EF hands.
AAC25423.1	AF072908	Nicotiana tabacum	calcium-dependent protein kinase. CDPK1.

AAF19402.1	AF203480	<i>Lycopersicon esculentum</i> phosphoenolpyruvate carboxylase kinase. protein kinase; member of Ca ²⁺ /CaM kinase family; lacks the autoinhibitory region and EF hands.
CAA65244.1	X95997	<i>Solanum tuberosum</i> SNF1-related protein kinase. PKIN1.
CAA57898.1	X82548	<i>Hordeum vulgare</i> SNF1-related protein kinase. BKIN2.
AAF19401.1	AF203479	<i>Glycine max</i> phosphoenolpyruvate carboxylase kinase. protein kinase; member of Ca ²⁺ /CaM kinase family; lacks the autoinhibitory region and EF hands.
AAD23582.1	AF128443	<i>Glycine max</i> probably involved in plant stress responses possibly regulates gene expression. SNF-1-like serine/threonine protein kinase. expressed in nodules, roots and leaves.
AAF34436.1	AF172282	<i>Oryza sativa</i> similar to mitogen-activated protein kinases. DUPR11.32.
BAA05648.1	D26601	<i>Nicotiana tabacum</i> protein kinase.
SEQ ID NO: 465		
CAB85467.1	AJ250316	<i>Brassica juncea</i> chloroplast omega-3 fatty acid desaturase. fad7.
BAA22441.1	D63954	<i>Zea mays</i> fatty acid desaturase. FAD7.
BAA11475.1	D79979	<i>Nicotiana tabacum</i> omega-3 fatty acid desaturase. NtFAD7.
AAA70334.1	U25817	<i>Sesamum indicum</i> omega-3 fatty acid desaturase. linoleic acid and hexadecadienoic acids desaturase.
AAB39387.1	U59477	<i>Perilla frutescens</i> omega-3 fatty acid desaturase.
CAA07638.1	AJ007739	<i>Solanum tuberosum</i> w-3 desaturase.
AAF27933.1	AF222989	<i>Capsicum annuum</i> omega-3 fatty acid desaturase. FAD.
AAB72241.1	U75745	<i>Petroselinum crispum</i> omega-3 fatty acid desaturase. complements the Arabidopsis fad7/8 fatty acid double mutant.
AAA61776.1	L22965	Chloroplast <i>Glycine soja</i> omega-3 fatty acid desaturase. Fadd.
AAF12821.1	AF200717	<i>Vernicia fordii</i> TnDES2. omega-3 fatty acid desaturase.
AAA86690.1	U17063	<i>Limnanthes douglasii</i> linoleic acid desaturation. delta-15 lineoyl desaturase. omega-3-fatty acid desaturase.
AAA73511.1	L25897	<i>Ricinus communis</i> desaturates linoleate to alpha-linolenate. linoleoyl desaturase. fad7. putative.

CAC18722.1	AJ302017	<i>Picea abies</i>	putative plastidial w-3 fatty acid desaturase. fad3.
AAD13527.1	AF061027	<i>Vernicia fordii</i>	omega-3 fatty acid desaturase precursor.
BAA22442.1	D84409	<i>Zea mays</i>	fatty acid desaturase. FAD8.
BAA22440.1	D63953	<i>Zea mays</i>	fatty acid desaturase. FAD8.
BAA07785.2	D43688	<i>Triticum aestivum</i>	plastid omega-3 fatty acid desaturase. TaFAD7.
AAA61774.1	L22963	Chloroplast <i>Brassica napus</i>	omega-3 fatty acid desaturase. Fadd.
AAC98967.1	AF047172	<i>Vernicia fordii</i>	omega-3 fatty acid desaturase. Fad3.
CAB45155.1	AJ011004	<i>Vernicia fordii</i>	omega-3 desaturase.
AAC16443.1	AF020204	<i>Pelargonium x hortorum</i>	omega-3 desaturase. pxh-15.
AAA61775.1	L22962	<i>Brassica napus</i>	omega-3 fatty acid desaturase. Fad3.
AAA61777.1	L22964	Chloroplast <i>Glycine soja</i>	omega-3 fatty acid desaturase. Fad3.
AAA32994.1	L01418	<i>Brassica napus</i>	desaturation of linoleic acid to linolenic acid. linoleic acid desaturase. fad3.
AAD15744.1	AF047039	<i>Perilla frutescens</i>	omega-3 fatty acid desaturase. FAD3.
BAA28358.1	D84678	<i>Triticum aestivum</i>	omega-3 fatty acid desaturase. TaFAD3.
BAA05515.1	D26509	<i>Nicotiana tabacum</i>	desaturation of dienoic fatty acid. microsomal omega-3 acid desaturase. NtFAD3.
BAA11397.1	D78506	<i>Oryza sativa</i>	w-3 fatty acid desaturase.
BAB18135.1	AB051215	<i>Glycine max</i>	microsomal omega-3 fatty acid desaturase.
BAA22439.1	D63952	<i>Zea mays</i>	fatty acid desaturase. FAD7.
BAA11396.1	D78505	<i>Oryza sativa</i>	w-3 fatty acid desaturase.
CAB71341.1	AJ250664	<i>Hordeum vulgare</i>	omega-3 fatty acid desaturase. bci-8.
AAD48897.1	AF083613	<i>Dunaliella salina</i>	omega-3 fatty acid desaturase. des3-1.

AAF80560.1	AF192486	Sesamum indicum	omega-6 fatty acid desaturase. FAD2.
CAB64256.1	AJ245938	Calendula officinalis	production of calendic acid. (8,11)-linoleoyl desaturase. des8.11.
AAB80696.1	U86072	Petroselinum crispum	omega-6 fatty acid desaturase. functional expression in yeast results in the formation of dienoic fatty acids (18:2 and 16:2).
SEQ ID NO: 467			
CAA60016.1	X86021	Solanum tuberosum	potassium channel. SKT1 gene. putative start codon.
CAA65254.1	X96390	Lycopersicon esculentum	potassium channel. LKT1.
AAF36832.1	AF207745	Triticum aestivum	AKT1-like potassium channel. TaAKT1.
CAA68912.1	Y07632	Zea mays	potassium channel. ZMK1.
AAF81249.1	AF267753	Mesembryanthemum crystallinum	putative potassium channel protein Mkt1p.
CAC05489.1	AJ271447	Populus tremula x Populus tremuloides	potassium channel. potassium channel 2. ptk2.
AAD16278.1	AF099095	Samanea saman	pulvinus inward-rectifying channel for potassium SPICK1. similar to Arabidopsis potassium channel AKT3.
CAB54856.1	AJ132686	Zea mays	potassium channel protein ZMK2. ZMK2.
CAA70870.1	Y09699	Solanum tuberosum	putative inward rectifying potassium channel. SKT2.
CAA71598.1	Y10579	Vicia faba	potassium channel.
BAA84085.1	AB032074	Nicotiana paniculata	potassium channel. NpKT1.
CAA12645.1	AJ225805	Egeria densa	inward potassium channel alpha subunit. homologous to the sequences of the family of inwardly rectifying potassium channels in plants which is structurally related to the shaker family of outwardly rectifying channels in Drosophila.
AAD39492.1	AF145272	Samanea saman	pulvinus inward-rectifying channel SPICK2. potassium channel; similar to AKT2/3.
CAC10514.1	AJ299019	Samanea saman	potassium release. outwardly rectifying potassium channel. spork1.
CAC05488.1	AJ271446	Populus tremula x Populus tremuloides	potassium channel. outward rectifying potassium channel. ptork.
AAF81251.1	AF267755	Mesembryanthemum crystallinum	potassium channel protein Mkt2p.

CAA70900.1	Y09753	Secale cereale	potassium channel. encodes membrane spanning domains H5-S6.
CAA70899.1	Y09752	Secale cereale	potassium channel. encodes membrane spanning domains H5-S6.
CAA70947.1	Y09818	Solanum tuberosum	putative inward rectifying potassium channel. SKT3.
CAA70895.1	Y09748	Hordeum vulgare	potassium channel. encodes membrane spanning domains H5-S6.
CAA70894.1	Y09747	Zea mays	potassium channel. encodes membrane spanning domains H5-S6.
CAA70896.1	Y09749	Vicia faba	potassium channel. encodes membrane spanning domains H5-S6.
CAA70897.1	Y09750	Plantago major	potassium channel. encodes membrane spanning domains H5-S6.
AAF33670.1	AF079872	Nicotiana tabacum	cyclic nucleotide-gated calmodulin-binding ion channel. CBP4.
AAF33669.1	AF079871	Nicotiana tabacum	cyclic nucleotide-gated calmodulin-binding ion channel. CBP7.
CAA05637.1	AJ002610	Hordeum vulgare	putative calmodulin binding transporter protein. CBT1.
CAA70898.1	Y09751	Plantago major	potassium channel. encodes membrane spanning domains H5-S6.
AAK16188.1	AC079887	Oryza sativa	putative cyclic nucleotide and calmodulin-regulated ion channel protein. OSJNBa0040E01.13.
SEQ ID NO: 468			
AAF76226.1	AF272572	Populus x canescens	14-3-3 protein. 14-3-3P20-1.
AAC04811.1	AF037460	Fritillaria agrestis	GF14 protein. GRF.
AAB40395.1	U80070	Mesembryanthemum crystallinum	G-box binding factor. 14-3-3-like protein. GBF.
AAF05737.1	AF191746	Lilium longiflorum	14-3-3-like protein.
AAB07457.1	U65957	Oryza sativa	GF14-c protein. rice 14-3-3 protein homolog; osGF14c.
AAB09580.1	U70533	Glycine max	SGF14A. 14-3-3 related protein.
AAA99431.1	L29150	Lycopersicon esculentum	14-3-3 protein homologue.
CAA74592.1	Y14200	Hordeum vulgare	14-3-3 protein.

AAB33304.1	S77133	Zea mays	GF14-6. GRF1. 14-3-3 protein homolog; This sequence comes from Fig. 5.
CAA66309.1	X97724	Solanum tuberosum	14-3-3 protein. leaf specific.
AAB07456.1	U65956	Oryza sativa	GF14-b protein. rice 14-3-3 protein homolog; osGF14b.
AAD27823.2	AF121194	Populus x canescens	14-3-3 protein. 14-3-3P20-2.
AAC49894.1	U91726	Nicotiana tabacum	14-3-3 isoform e. T14-3e.
CAA44259.1	X62388	Hordeum vulgare	14-3-3 protein homologue.
AAD27827.2	AF121198	Picea glauca	14-3-3 protein. 14-3-3EB9D.
CAA63658.1	X93170	Hordeum vulgare	Hv14-3-3b.
CAB42546.2	AJ238681	Pisum sativum	14-3-3-like protein. 14-3-3.
AAA33505.1	M96856	Zea mays	regulatory protein. GF14-12.
AAA85817.1	U15036	Pisum sativum	14-3-3-like protein.
AAK26634.1	AF342780	Brassica napus	GF14 omega. 14-3-3 protein.
CAA72094.1	Y11211	Nicotiana tabacum	14-3-3-like protein B.
CAA72383.1	Y11687	Solanum tuberosum	14-3-3 protein. 34G.
AAC49892.1	U91724	Nicotiana tabacum	14-3-3 isoform c. T14-3c.
CAA53700.1	X76086	Cucurbita pepo	14-3-3 protein 32kDa endonuclease. A215. single polypeptide.
CAA72382.1	Y11686	Solanum tuberosum	14-3-3 protein. 30G.
CAB42547.1	AJ238682	Pisum sativum	14-3-3-like protein. 14-3-3.
CAA65147.1	X95902	Lycopersicon esculentum	14-3-3 protein. tft3 gene.
AAC49891.1	U91723	Nicotiana tabacum	14-3-3 isoform b. T14-3b.
AAB07458.1	U65958	Oryza sativa	GF14-d protein. rice 14-3-3 protein homolog; osGF14d.

CAA72381.1	Y11685	Solanum tuberosum	14-3-3 protein. 16R.
AAC49895.1	U91727	Nicotiana tabacum	14-3-3 isoform f. T14-3f.
CAA72095.1	Y11212	Nicotiana tabacum	14-3-3-like protein A.
BAB11739.1	AB042193	Triticum aestivum	TaWIN1. TaWIN1. TaWIN1 is a member of 14-3-3 protein family.
CAA65146.1	X95901	Lycopersicon esculentum	14-3-3 protein. tft2 gene.
CAA65148.1	X95903	Lycopersicon esculentum	14-3-3 protein. tft5 gene.
AAC17447.1	AF066076	Helianthus annuus	14-3-3-like protein.
CAA60800.1	X87370	Solanum tuberosum	14-3-3 protein. RA215. root specific.
CAA55964.1	X79445	Chlamydomonas reinhardtii	14-3-3 protein.
CAC03467.1	Y19105	Chlamydomonas reinhardtii	14-3-3 protein.
CAA65149.1	X95904	Lycopersicon esculentum	14-3-3 protein. tft6 gene.
CAB65693.1	AJ270959	Lycopersicon esculentum	tft3 14-3-3 protein. tft3.
BAB11740.1	AB042194	Triticum aestivum	TaWIN2. TaWIN2. TaWIN2 is a member of 14-3-3 protein family.
AAA99430.1	L29151	Lycopersicon esculentum	14-3-3 protein homologue.
CAA72384.1	Y11688	Solanum tuberosum	14-3-3 protein. 35G.
CAA65145.1	X95900	Lycopersicon esculentum	14-3-3 protein. tft1 gene.
AAC49893.1	U91725	Nicotiana tabacum	14-3-3 isoform d. T14-3d.
SEQ ID NO: 470			
AAA19701.1	L24438	Thlaspi arvense	cytochrome P450.
AAA32913.1	M32885	Persea americana	cytochrome P-450LXXIA1 (cyp71A1).
AAC39318.1	AF029858	Sorghum bicolor	second multifunctional cytochrome P450 in the biosynthetic pathway of the cyanogenic glucoside dhurrin. Catalyzes the conversion of p-hydroxyphenylacetaldoxime to p-hydroxymandelonitrile. cytochrome P450 CYP71E1. CYP71E1. No EST#s identified.

BAB40323.1	AB037244	Asparagus officinalis cytochrome P450. ASPI-1.
BAB40324.1	AB037245	Asparagus officinalis cytochrome P450. ASPI-2.
AAB94589.1	AF022460	Glycine max CYP83D1p. CYP83D1. cytochrome P450 monooxygenase.
CAA70575.1	Y09423	Nepeta racemosa cytochrome P450. CYP71A5.
CAA70576.1	Y09424	Nepeta racemosa cytochrome P450. CYP71A6.
CAA71513.1	Y10489	Glycine max putative cytochrome P450.
AAB61965.1	U48435	Solanum chacoense putative cytochrome P450.
AAB94588.1	AF022459	Glycine max CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.
CAA50312.1	X70981	Solanum melongena P450 hydroxylase. CYPEG2.
CAA71514.1	Y10490	Glycine max putative cytochrome P450.
AAB94584.1	AF022157	Glycine max capable of catalyzing the metabolism of phenylurea herbicides. CYP71A10. CYP71A10. cytochrome P450 monooxygenase.
AAD47832.1	AF166332	Nicotiana tabacum cytochrome P450.
AAF27282.1	AF122821	Capsicum annuum cytochrome P450. PepCYP.
CAA71517.1	Y10493	Glycine max putative cytochrome P450.
CAA83941.1	Z33875	Mentha x piperita cytochrome P-450 oxidase.
CAB56503.1	AJ238612	Catharanthus roseus cytochrome P450.
AAB61964.1	U48434	Solanum chacoense putative cytochrome P450.
AAB69644.1	AF000403	Lotus japonicus putative cytochrome P450. LjNP450.
CAA50645.1	X71654	Solanum melongena P450 hydroxylase.
BAA03635.1	D14990	Solanum melongena Cytochrome P-450EG4.
AAD44151.1	AF124816	Mentha x piperita cytochrome p450 isoform PM17.

AAD44150.1	AF124815	Mentha spicata cytochrome p450.
AAD44152.1	AF124817	Mentha x piperita cytochrome p450 isoform PM2.
BAB39252.1	AP002968	Oryza sativa putative cytochrome P450. P0416G11.1.
AAK38084.1	AF321860	Lolium rigidum putative cytochrome P450.
AAK38083.1	AF321859	Lolium rigidum putative cytochrome P450.
AAK38087.1	AF321863	Lolium rigidum putative cytochrome P450.
AAK38082.1	AF321858	Lolium rigidum putative cytochrome P450.
CAC27827.1	AJ295719	Catharanthus roseus geraniol hydroxylase. cytochrome P450. cyp71.
AAB94587.1	AF022458	Glycine max CYP98A2p. CYP98A2. cytochrome P450 monooxygenase.
AAK38088.1	AF321864	Lolium rigidum putative cytochrome P450.
AAD37433.1	AF150881	Lycopersicon esculentum x Lycopersicon peruvianum catalyzes the hydroxylation of ferulic acid to 5-hydroxyferulic acid. ferulate-5-hydroxylase. CYP84. cytochrome P450-dependent monooxygenase; F5H; FAH1.
AAG14963.1	AF214009	Brassica napus cytochrome p450-dependent monooxygenase. BNF5H3.
CAA57425.1	X81831	Zea mays cytochrome P450. CYP71C4. family CYP71, subfamily CYP71C.
CAA72196.1	Y11368	Zea mays cytochrome p450. cyp71c4.
AAG44132.1	AF218296	Pisum sativum cytochrome P450. P450 isolog.
AAG14962.1	AF214008	Brassica napus cytochrome p450-dependent monooxygenase. BNF5H2.
AAG14961.1	AF214007	Brassica napus cytochrome p450-dependent monooxygenase. BNF5H1.
AAD56282.1	AF155332	Petunia x hybrida flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.
SEQ ID NO: 471		
AAD17855.1	AF099111	Zea mays sigma factor. sig2. putative sigma subunit of chloroplast Escherichia coli-like RNA polymerase; Sig2.
SEQ ID NO: 472		

AAD45623.1	AF084185	Brassica napus	dehydration responsive element binding protein. DNA binding protein; DRE binding protein.
AAG43549.1	AF211531	Nicotiana tabacum	Avr9/Cf-9 rapidly elicited protein 111B. ACRE111B. similar to EREBP transcription factors.
AAG43548.1	AF211530	Nicotiana tabacum	Avr9/Cf-9 rapidly elicited protein 111A. ACRE111A. similar to EREBP transcription factors.
AAK01089.1	AF298231	Hordeum vulgare	CBF3-like protein BCBF3. BCBF3. AP2 domain protein; DRE binding factor.
AAG59618.1	AF239616	Hordeum vulgare	CRT/DRE-binding factor. CBF.
AAK01088.1	AF298230	Hordeum vulgare	CBF1-like protein BCBF1. BCBF1. AP2 domain protein; putative DRE binding factor.
AAG59619.1	AF243384	Oryza sativa	CRT/DRE binding factor. CBF. DREB.
AAK31271.1	AC079890	Oryza sativa	putative transcriptional factor. OSJNBb0089A17.22.
CAC12822.1	AJ299252	Nicotiana tabacum	AP2 domain-containing transcription factor. ap2.
BAA76734.1	AB024575	Nicotiana tabacum	ethylene responsive element binding factor.
AAC29516.1	U77655	Solanum tuberosum	DNA binding protein homolog. STWAAEIRD.
AAF23899.1	AF193803	Oryza sativa	transcription factor EREBP1. EREBP/AP2-like transcription factor.
CAB93939.1	AJ238739	Catharanthus roseus	putative transcription factor. AP2-domain DNA-binding protein. orcal.
BAB16083.1	AB036883	Oryza sativa	transcriptional repressor. osERF3. osERF3. ERF protein family ERF3 associated repression domain.
BAB03248.1	AB037183	Oryza sativa	ERF protein transcriptional repressor. ethylene responsive element binding factor3. osERF3.
BAA97124.1	AB016266	Nicotiana sylvestris	ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf4.
BAA97123.1	AB016265	Nicotiana sylvestris	ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf3.
AAG43545.1	AF211527	Nicotiana tabacum	Avr9/Cf-9 rapidly elicited protein 1. ACRE1. similar to EREBP transcription factors.
AAD00708.1	U91857	Stylosanthes hamata	ethylene-responsive element binding protein homolog. similar to EREBP1, -2, -3 and -4 proteins encoded by GenBank Accession Numbers D38123, D38126, D38124, and D38125 respectively.

AAC49741.1	U89257	Lycopersicon esculentum	DNA-binding protein binds the GCC box pathogenesis-related promoter element. Pti6.
AAG60182.1	AC084763	Oryza sativa	putative ethylene-responsive element binding protein. OSJNBa0027P10.12.
AAK31279.1	AC079890	Oryza sativa	putative ethylene-responsive element binding protein. OSJNBb0089A17.16.
AAC14323.1	AF058827	Nicotiana tabacum	TSI1. Tsi1. contains putative AP2 DNA-binding domain; similar to Pti6.
AAC50047.1	U89255	Lycopersicon esculentum	binds the GCC box pathogenesis-related promoter element DNA-binding protein. Pti4.
BAA97122.1	AB016264	Nicotiana sylvestris	ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf2.
CAB96899.1	AJ251249	Catharanthus roseus	transcription factor. AP2-domain DNA-binding protein. orca3.
CAB93940.1	AJ238740	Catharanthus roseus	putative transcription factor. AP2-domain DNA-binding protein. orca2.
AAF63205.1	AF245119	Mesembryanthemum crystallinum	AP2-related transcription factor. CDBP. stress induced transcription factor.
BAA87068.1	AB035270	Matricaria chamomilla	ethylene-responsive element binding protein1 homolog. McEREBP1.
CAB96900.1	AJ251250	Catharanthus roseus	transcription factor. AP2-domain DNA-binding protein. orca3.
BAB21218.1	AP002913	Oryza sativa	putative DNA binding protein RAV2. P0480E02.24.
BAA07321.1	D38123	Nicotiana tabacum	ERF1. ethylene-responsive transcription factor.
AAC49740.1	U89256	Lycopersicon esculentum	binds the GCC box pathogenesis-related promoter element DNA-binding protein. Pti5.
AAB38748.1	U81157	Nicotiana tabacum	S25-XP1 DNA binding protein.
BAB21211.1	AP002913	Oryza sativa	putative DNA binding protein RAV2. P0480E02.17.
SEQ ID NO: 473			
BAA85438.1	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683).
AAK00436.1	AC060755	Oryza sativa	putative zinc finger protein. OSJNBa0003O19.23.
AAG43550.1	AF211532	Nicotiana tabacum	Avr9/Cf-9 rapidly elicited protein 132. ACRE132. similar to RING finger proteins.
SEQ ID NO: 475			
AAG43550.1	AF211532	Nicotiana tabacum	Avr9/Cf-9 rapidly elicited protein 132. ACRE132. similar to RING finger proteins.

BAA78746.1	AB023482	Oryza sativa	Similar to Arabidopsis thaliana RING-H2 finger protein RHX1a mRNA, partial cds.(AF079184).
BAA96875.1	AB045121	Oryza sativa	RING finger 1. RRF1.
CAA74911.1	Y14573	Hordeum vulgare	ring finger protein. putative.
AAK00436.1	AC060755	Oryza sativa	putative zinc finger protein. OSJNBa0003O19.23.
AAG46117.1	AC073166	Oryza sativa	putative ring finger protein. OSJNBb0064P21.7.
BAA90357.1	AP001080	Oryza sativa	EST AU070319(S10788) corresponds to a region of the predicted gene. Similar to RING-H2 finger protein RHA2b (AC006200).
BAA77204.1	AB026262	Cicer arietinum	ring finger protein.
BAA90806.1	AP001168	Oryza sativa	ESTs C26000(C11448),AU082130(C11448) correspond to a region of the predicted gene.; Similar to mRNA for zinc-finger protein (Z36749).
SEQ ID NO: 476			
BAA78764.1	AB023482	Oryza sativa	ESTs C98382(C2985),D22444(C11129) correspond to a region of the predicted gene.; Similar to Arabidopsis thaliana APK1 gene for protein tyrosine-serine-threonine kinase.(D12522).
AAK11674.1	AF339747	Lophopyrum elongatum	protein kinase. ESI47.
AAF43496.1	AF131222	Lophopyrum elongatum	protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.
AAG16628.1	AY007545	Brassica napus	protein serine/threonine kinase BNK1.
BAA94509.1	AB041503	Populus nigra	protein kinase 1. PnPK1.
BAA94510.1	AB041504	Populus nigra	protein kinase 2. PnPK2.
BAB07999.1	AP002525	Oryza sativa	putative protein kinase. P0462H08.22. contains EST C22619(S11214).
BAB03429.1	AP002817	Oryza sativa	EST C22619(S11214) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).
BAA87853.1	AP000816	Oryza sativa	EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).

BAB16871.1	AP002537	Oryza sativa	putative protein kinase APK1A Arabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192), D25110(R3192).
BAB39409.1	AP002901	Oryza sativa	putative protein kinase. P0456F08.9. contains EST C23560(R0290).
AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.
BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808), AU056702(S20808).
CAB51834.1	00069	Oryza sativa	11332.5. contains eukaryotic protein kinase domain PF.
BAB21240.1	AP002953	Oryza sativa	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461), C22360(C11461).
AAK21965.1	AY028699	Brassica napus	receptor protein kinase PERK1.
AAG59657.1	AC084319	Oryza sativa	putative protein kinase. OSJNBa0004B24.20.
AAG03090.1	AC073405	Oryza sativa	Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).
AAG25966.1	AF302082	Nicotiana tabacum	cytokinin-regulated kinase 1. CRK1. protein kinase; transcript abundance decreases rapidly after cytokinin treatment.
BAB21241.1	AP002953	Oryza sativa	Putative Pto kinase interactor 1. P0426D06.21. contains ESTs AU108280(E0721), D48017(S13927).
CAB51480.1	Y14600	Sorghum bicolor	putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.
AAC61805.1	U28007	Lycopersicon esculentum	serine/threonine protein kinase. Pto kinase interactor 1. Pti1. Pti1 kinase.
BAA87852.1	AP000816	Oryza sativa	Similar to putative Ser/Thr protein kinase. (AC004218).
BAA92221.1	AP001278	Oryza sativa	Similar to Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).
AAB09771.1	U67422	Zea mays	CRINKLY4 precursor. cr4. receptor kinase homolog.
BAA90808.1	AP001168	Oryza sativa	Similar to putative receptor-like protein kinase (AL035679).
AAC27894.1	AF023164	Zea mays	leucine-rich repeat transmembrane protein kinase 1. ltk1.
AAB61708.1	U93048	Daucus carota	somatic embryogenesis receptor-like kinase. SERK.

AAF91336.1	AF249317	Glycine max Ptil kinase-like protein. Ptila. protein kinase.
AAF91337.1	AF249318	Glycine max Ptil kinase-like protein. Ptilb. protein kinase.
AAG33377.1	AF290411	Oryza meyeriana serine/threonine protein kinase. R1.
AAC27895.1	AF023165	Zea mays leucine-rich repeat transmembrane protein kinase 2. Itk2.
AAK11566.1	AF318490	Lycopersicon hirsutum Pto-like protein kinase E. LhirPtoE. confers resistance to bacterial speck disease.
CAA97692.1	Z73295	Catharanthus roseus receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
AAF34428.1	AF172282	Oryza sativa receptor-like protein kinase. DUPR11.18.
AAF76306.1	AF220602	Lycopersicon pimpinellifolium Pto kinase.
AAB47423.1	U59315	Lycopersicon pimpinellifolium serine/threonine protein kinase Pto. Pto. bacterial speck disease resistance in tomato; disease resistance gene.
AAC48914.1	U02271	Lycopersicon pimpinellifolium protein kinase.
AAK11567.1	AF318491	Lycopersicon hirsutum Pto-like protein kinase F. LhirPtoF.
AAB47421.1	U59316	Lycopersicon esculentum serine/threonine protein kinase Pto. pto. allele of Pto bacterial speck disease resistance gene in tomato.
AAF76313.1	AF220603	Lycopersicon esculentum Pto kinase. LescPth5.
AAF66615.1	AF142596	Nicotiana tabacum LRR receptor-like protein kinase.
BAA92954.1	AP001551	Oryza sativa Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).
BAA92953.1	AP001551	Oryza sativa Similar to Arabidopsis thaliana chromosome 4 BAC clone F10M6 ; S-receptor kinase -like protein. (AL021811).
SEQ ID NO: 479		
CAA42622.1	X60007	Nicotiana glauca nsGRP-2. putative glycine-rich protein of 19.7kDa.
SEQ ID NO: 480		
BAA83373.1	AP000391	Oryza sativa ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).

BAA84787.1	AP000559	Oryza sativa	ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).
AAF91324.1	AF244890	Glycine max	receptor-like protein kinase 3. RLK3. GmRLK3.
AAF91322.1	AF244888	Glycine max	receptor-like protein kinase 1. RLK1. GmRLK1.
AAF91323.1	AF244889	Glycine max	receptor-like protein kinase 2. RLK2. GmRLK2.
AAB36558.1	U77888	Ipomoea nil	receptor-like protein kinase INRPK1. inrpk1. leucine-rich repeat.
AAC36318.1	AF053127	Malus x domestica	leucine-rich receptor-like protein kinase. LRPKml.
AAF59906.1	AF197947	Glycine max	receptor protein kinase-like protein. CLV1B.
BAB40094.1	AP003210	Oryza sativa	putative receptor protein kinase. OSJNBa0010K01.7.
AAF59905.1	AF197946	Glycine max	receptor protein kinase-like protein. CLV1A.
CAC20842.1	AJ250467	Pinus sylvestris	receptor protein kinase. upk.
BAB03629.1	AP002522	Oryza sativa	putative protein kinase Xa21. P0009G03.30.
BAB03621.1	AP002522	Oryza sativa	putative protein kinase Xa21. P0009G03.21.
BAB03631.1	AP002522	Oryza sativa	putative protein kinase Xa21. P0009G03.32.
AAB82755.1	U72725	Oryza longistaminata	receptor kinase-like protein. Xa21 gene family member A1; downstream of microsatellite region; disease resistance gene family member.
AAF34426.1	AF172282	Oryza sativa	leucine rich repeat containing protein kinase. DUPR11.16.
AAK27806.1	AC022457	Oryza sativa	putative protein kinase. OSJNBa0006L06.21.
CAA61510.1	X89226	Oryza sativa	leucine-rich repeat/receptor protein kinase. lrk2.
AAC49123.1	U37133	Oryza sativa	receptor kinase-like protein. Xa21. Xa21 disease resistance gene.
AAC80225.1	U72723	Oryza longistaminata	receptor kinase-like protein. Xa21. disease resistance gene.
AAK27817.1	AC022457	Oryza sativa	putative protein kinase. OSJNBa0006L06.16.

BAA82393.1 AP000367 *Oryza sativa*
EST C96716(C10608) corresponds to a region of the predicted gene.; Similar to putative
receptor protein kinase. (AC002334).

BAB03627.1 AP002522 *Oryza sativa*
putative protein kinase Xa21. P0009G03.27.

AAB82756.1 U72724 *Oryza sativa*
receptor kinase-like protein. Xa21 gene family member E.

AAG52992.1 U77888 *Ipomoea nil*
receptor-like protein kinase INRPK1a. inrpk1.

BAA88636.1 AB029327 *Nicotiana tabacum*
elicitor-inducible LRR receptor-like protein EILP. EILP.

AAB82753.1 U72726 *Oryza longistaminata*
receptor kinase-like protein. Xa21 gene family member D.

AAG52994.1 U77888 *Ipomoea nil*
receptor-like protein kinase INRPK1c. inrpk1.

CAB51480.1 Y14600 *Sorghum bicolor*
putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.

AAK21965.1 AY028699 *Brassica napus*
receptor protein kinase PERK1.

SEQ ID NO: 481

CAB43505.1 AJ239051 *Cicer arietinum*
cytochrome P450. cyp81E2.

BAA22422.1 AB001379 *Glycyrrhiza echinata*
cytochrome P450. CYP81E1.

BAA93634.1 AB025016 *Lotus japonicus*
cytochrome P450.

BAA74465.1 AB022732 *Glycyrrhiza echinata*
cytochrome P450. CYP Ge-31.

CAB41490.1 AJ238439 *Cicer arietinum*
cytochrome P450 monooxygenase. cyp81E3v2.

CAA10067.1 AJ012581 *Cicer arietinum*
cytochrome P450. cyp81E3.

CAA04117.1 AJ000478 *Helianthus tuberosus*
fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1l. chimeric sequence (from 5'-
race).

CAA04116.1 AJ000477 *Helianthus tuberosus*
fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1c.

AAK38080.1 AF321856 *Lolium rigidum*
putative cytochrome P450.

AAK38079.1 AF321855 *Lolium rigidum*
putative cytochrome P450.

AAK38081.1 AF321857 *Lolium rigidum*
putative cytochrome P450.

AAG09208.1	AF175278	<i>Pisum sativum</i> wound-inducible P450 hydroxylase. CYP82A1.
CAA71876.1	Y10982	<i>Glycine max</i> putative cytochrome P450.
AAC49188.2	U29333	<i>Pisum sativum</i> cytochrome P450 monooxygenase. CYP82. new cytochrome P450 family.
CAA65580.1	X96784	<i>Nicotiana tabacum</i> cytochrome P450. hsr515.
CAA71515.1	Y10491	<i>Glycine max</i> putative cytochrome P450.
BAA92894.1	AB006790	<i>Petunia x hybrida</i> cytochrome P450. IMT-2.
AAG44132.1	AF218296	<i>Pisum sativum</i> cytochrome P450. P450 isolog.
CAA64635.1	X95342	<i>Nicotiana tabacum</i> cytochrome P450. hsr515. hypersensitivity-related gene.
AAD56282.1	AF155332	<i>Petunia x hybrida</i> flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.
AAC34853.1	AF082028	<i>Hemerocallis hybrid cultivar</i> putative cyt P450-containing fatty acid hydroxylase. senescence-associated protein 3. SA3. mRNA accumulates in senescing petals.
BAA12159.1	D83968	<i>Glycine max</i> Cytochrome P-450 (CYP93A1).
AAA32913.1	M32885	<i>Persea americana</i> cytochrome P-450LXXIA1 (cyp71A1).
CAA70575.1	Y09423	<i>Nepeta racemosa</i> cytochrome P450. CYP71A5.
AAG34695.1	AF313492	<i>Matthiola incana</i> putative cytochrome P450.
CAA71877.1	Y10983	<i>Glycine max</i> putative cytochrome P450.
CAA71516.1	Y10492	<i>Glycine max</i> putative cytochrome P450.
AAB94587.1	AF022458	<i>Glycine max</i> CYP98A2p. CYP98A2. cytochrome P450 monooxygenase.
AAC39454.1	AF014802	<i>Eschscholzia californica</i> (S)-N-methylcoclaurine 3'-hydroxylase. CYP82B1. cytochrome P-450-dependent monooxygenase; methyl jasmonate-inducible cytochrome P-450-dependent, homologous to wound-inducible CYP82A1 of <i>Pisum sativum</i> GenBank Accession Number U29333.
CAA70576.1	Y09424	<i>Nepeta racemosa</i> cytochrome P450. CYP71A6.
AAB94590.1	AF022461	<i>Glycine max</i> CYP82C1p. CYP82C1. cytochrome P450 monooxygenase.

BAB40323.1 AB037244 *Asparagus officinalis*
cytochrome P450. ASPI-1.

BAB40324.1 AB037245 *Asparagus officinalis*
cytochrome P450. ASPI-2.

AAB61965.1 U48435 *Solanum chacoense*
putative cytochrome P450.

AAA19701.1 L24438 *Thlaspi arvense*
cytochrome P450.

BAA84071.1 AB028151 *Antirrhinum majus*
flavone synthase II. cytochrome P450. AFNS2.

BAA13076.1 D86351 *Glycine max*
cytochrome P-450 (CYP93A2).

AAD38930.1 AF135485 *Glycine max*
cytochrome P450 monooxygenase CYP93D1. CYP93E1.

AAC32274.1 AF081575 *Petunia x hybrida*
flavonoid 3',5'-hydroxylase. Hfl. P450 enzyme.

SEQ ID NO: 487

BAA96181.1 AP002093 *Oryza sativa*
EST AU056651(S20760) corresponds to a region of the predicted gene. Similar to
Arabidopsis thaliana chromosome II BAC F19I3; putative amino acid transporter
(AC004238).

BAA96139.1 AP002092 *Oryza sativa*
EST AU056651(S20760) corresponds to a region of the predicted gene. Similar to
Arabidopsis thaliana chromosome II BAC F19I3; putative amino acid transporter
(AC004238).

SEQ ID NO: 495

AAB71528.1 U94784 *Helianthus annuus*
ATPase. unconventional myosin. hamy4. Hamyo4.

AAB71529.1 U94785 *Helianthus annuus*
ATPase. unconventional myosin. hamy5. Hamyo5.

AAB71527.1 U94782 *Helianthus annuus*
ATPase. unconventional myosin. hamy2. Hamyo2.

AAD17931.2 AF104924 *Zea mays*
unconventional myosin heavy chain. MYO1. ATPase; similar to myosin class XI.

AAC27525.1 AF077352 *Chlamydomonas reinhardtii*
myosin heavy chain. MYO1. class XI.

AAK21311.1 AF338254 *Petroselinum crispum*
myosin subfamily XI heavy chain. PCM3.

BAA87057.1 AB034154 *Chara corallina*
unconventional myosin heavy chain. ccm.

BAB03273.1 AB007459 *Chara corallina*
cytoplasmic streaming. myosin. ccm1. CCM1.

AAF43440.1	AF233886	Vallisneria gigantea	unconventional myosin XI. VMYO1.
AAB53062.1	U94398	Acetabularia cliftonii	myosin. myo2.
AAD34597.1	AF147739	Zea mays	myosin XI. M2. unconventional myosin.
AAB53061.1	U94397	Acetabularia cliftonii	myosin. myo1.
AAD31926.1	AF147738	Zea mays	myosin VIII ZMM3. zmm3. unconventional myosin.
AAB71526.1	U94781	Helianthus annuus	unconventional myosin. hamy1. homologous to ATM1.
AAG49341.1	AF319457	Petroselinum crispum	myosin subfamily VIII heavy chain.
AAB93521.1	U94783	Helianthus annuus	unconventional myosin. hamy3. Hamyo3; similar to class VIII myosin.
CAA47476.1	X67102	Anemia phyllitidis	myosin heavy chain. myo15.
CAA47477.1	X67103	Anemia phyllitidis	myosin heavy chain. myo22.
AAF43441.1	AF233887	Vallisneria gigantea	unconventional myosin VIII. VMYO2.
AAG13633.1	AC078840	Oryza sativa	putative myosin. OSJNBb0073N24.16.
AAA92120.1	U48785	Vigna mungo	plant myosin MBM1. mbm1. head coding region.
SEQ ID NO: 496			
AAA34138.1	M96324	Lycopersicon esculentum	The calcium ATPase is a calcium ion pump. Ca ²⁺ -ATPase. LCA1.
AAD11618.1	AF050496	Lycopersicon esculentum	Ca ²⁺ -ATPase. LCA1B; alternative transcript.
AAD11617.1	AF050495	Lycopersicon esculentum	Ca ²⁺ -ATPase. LCA1A; alternative transcript.
BAA90510.2	AP001111	Oryza sativa	rice EST AU030811, similar to rice Ca ²⁺ -ATPase (U82966).
CAA63790.1	X93592	Dunaliella bioculata	P-type ATPase. cal. calcium pumping; CA1.
AAB58910.1	U82966	Oryza sativa	Ca ²⁺ -ATPase.
AAF73985.1	AF096871	Zea mays	calcium pump. calcium ATPase. cap1.

AAG28436.1	AF195029	Glycine max	plasma membrane Ca ²⁺ -ATPase. SCA2.
AAG28435.1	AF195028	Glycine max	plasma membrane Ca ²⁺ -ATPase. SCA1.
CAA68234.1	X99972	Brassica oleracea	calmodulin-stimulated calcium-ATPase.
AAD31896.1	AF145478	Mesembryanthemum crystallinum	calcium ATPase.
CAB85494.1	AJ132891	Medicago truncatula	proton pump. H ⁺ -ATPase. ha1.
CAB85495.1	AJ132892	Medicago truncatula	proton pump. H ⁺ -ATPase. ha1.
CAB69824.1	AJ271439	Prunus persica	plasma membrane H ⁺ ATPase. PPA1.
CAA52107.1	X73901	Dunaliella bioculata	plasma membrane ATPase. pma1.
AAD46188.1	AF156691	Nicotiana plumbaginifolia	plasma membrane proton ATPase. pma9.
BAA01058.1	D10207	Oryza sativa	H-ATPase. OSA1.
AAA34094.1	M80489	Nicotiana plumbaginifolia	plasma membrane H ⁺ ATPase. pma1.
AAA34098.1	M80490	Nicotiana plumbaginifolia	plasma membrane H ⁺ ATPase. pma3.
AAA34173.1	M60166	Lycopersicon esculentum	H ⁺ -ATPase. LHA1.
CAA54046.1	X76536	Solanum tuberosum	H(+)-transporting ATPase. PHA1.
AAD55399.1	AF179442	Lycopersicon esculentum	plasma membrane H ⁺ -ATPase isoform LHA2. LHA2.
AAB49042.1	U54690	Dunaliella acidophila	plasma membrane proton ATPase. dha1. DaDHA1; proton pump.
AAF98344.1	AF275745	Lycopersicon esculentum	plasma membrane H ⁺ -ATPase. LHA2. P-type ion pump.
BAA08134.1	D45189	Zostera marina	plasma membrane H ⁺ -ATPase. zha1.
AAA34052.1	M27888	Nicotiana plumbaginifolia	H ⁺ -translocating ATPase.
CAA59800.1	X85805	Zea mays	H(+)-transporting ATPase. MHA-2.
AAB17186.1	U72148	Lycopersicon esculentum	plasma membrane H ⁺ -ATPase. LHA4. plasma membrane proton pumping ATPase.

CAA54045.1	X76535	Solanum tuberosum	H(+)-transporting ATPase. PHA2.
CAB69823.1	AJ271438	Prunus persica	plasma membrane H ⁺ ATPase. PPA2.
BAA06629.1	D31843	Oryza sativa	plasma membrane H ⁺ -ATPase. OSA2.
CAC29435.1	AJ310523	Vicia faba	P-type H ⁺ -ATPase. vha4. predominantly expressed in flowers.
CAC29436.1	AJ310524	Vicia faba	P-type H ⁺ -ATPase. ha5. predominantly expressed in guard cells and flowers.
CAA59799.1	X85804	Phaseolus vulgaris	H(+)-transporting ATPase. BHA-1.
AAD46186.1	AF156679	Nicotiana plumbaginifolia	plasma membrane proton ATPase. pma6.
AAB84202.2	AF029256	Kosteletzkya virginica	plasma membrane proton ATPase. ATP1.
AAD46187.1	AF156683	Nicotiana plumbaginifolia	plasma membrane proton ATPase. pma8.
AAB60276.1	U09989	Zea mays	H(+)-transporting ATPase. Mha1.
AAB41898.1	U84891	Mesembryanthemum crystallinum	plasma membrane proton pump. H ⁺ -transporting ATPase. PMA.
AAB35314.2	S79323	Vicia faba	plasma membrane H(+)-ATPase precursor. plasma membrane H(+)-ATPase. This sequence comes from Fig. 1; conceptual translation presented here differs from translation in publication.
AAK31799.1	AY029190	Lilium longiflorum	plasma membrane H ⁺ ATPase. LILHA1.
CAA47275.1	X66737	Nicotiana plumbaginifolia	plasma membrane H ⁺ -ATPase. pma4.
BAA37150.1	AB022442	Vicia faba	p-type H ⁺ -ATPase. VHA2.
AAG01028.1	AF289025	Cucumis sativus	plasma membrane H ⁺ -ATPase.
AAA81348.1	U38965	Vicia faba	p-type H ⁺ -ATPase. VHA2.
AAK32118.1	AF308816	Hordeum vulgare	plasmalemma H ⁺ -ATPase 1.
AAF97591.1	AF263917	Lycopersicon esculentum	plasma membrane proton ATPase. LHA8.
AAK32119.1	AF308817	Hordeum vulgare	plasmalemma H ⁺ -ATPase 2.

AAA20601.1 U08985 Zea mays
plasma-membrane H⁺ ATPase. Zmpmal.

SEQ ID NO: 497

AAB41742.1 U82559 Lycopersicon esculentum
aldehyde oxidase 1 homolog. TAO1. has sequence properties of the molybdenum cofactor containing the hydroxylase genes aldehyde oxidase and xanthine dehydrogenase; belongs to a multigene family.

AAB41741.1 U82558 Lycopersicon esculentum
aldehyde oxidase 1 homolog. TAO1. has sequence properties of the molybdenum cofactor containing the hydroxylase genes aldehyde oxidase and xanthine dehydrogenase; belongs to a multigene family.

SEQ ID NO: 498

CAA73134.1 Y12531 Brassica oleracea
serine/threonine kinase. BRLK.

AAB93834.1 U82481 Zea mays
KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.

CAA67145.1 X98520 Brassica oleracea
receptor-like kinase. SFR2.

CAA74661.1 Y14285 Brassica oleracea
SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.

CAA73133.1 Y12530 Brassica oleracea
serine /threonine kinase. ARLK.

AAA62232.1 U00443 Brassica napus
S-receptor kinase. protein contains an immunoglobulin-like domain.

CAB89179.1 AJ245479 Brassica napus subsp. napus
ser /thr kinase. S-locus receptor kinase. srk.

AAA33008.1 M97667 Brassica napus
serine/threonine kinase receptor.

BAA92836.1 AB032473 Brassica oleracea
S18 S-locus receptor kinase. SRK18.

BAA23676.1 AB000970 Brassica rapa
receptor kinase 1. BcRK1.

AAC23542.1 U20948 Ipomoea trifida
receptor protein kinase. IRK1.

AAA33000.1 M76647 Brassica oleracea
receptor protein kinase. SKR6.

BAA21132.1 D88193 Brassica rapa
S-receptor kinase. SRK9 (B.c).

BAA06285.1 D30049 Brassica rapa
S-receptor kinase SRK9.

CAB41879.1	Y18260	Brassica oleracea	SRK15 protein. SRK15. receptor-like kinase.
BAA07577.2	D38564	Brassica rapa	receptor protein kinase SRK12.
CAA74662.1	Y14286	Brassica oleracea	SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
BAB21001.1	AB054061	Brassica rapa	S locus receptor kinase. SRK22.
BAA92837.1	AB032474	Brassica oleracea	S60 S-locus receptor kinase. SRK60.
CAB41878.1	Y18259	Brassica oleracea	SRK5 protein. SRK5. receptor-like kinase.
CAA79355.1	Z18921	Brassica oleracea	S-receptor kinase-like protein.
BAA07576.1	D38563	Brassica rapa	receptor protein kinase SRK8.
AAF34428.1	AF172282	Oryza sativa	receptor-like protein kinase. DUPR11.18.
AAD21872.1	AF078082	Phaseolus vulgaris	receptor-like protein kinase homolog RK20-1.
AAD52097.1	AF088885	Nicotiana tabacum	receptor-like kinase CHRK1. Chrk1.
BAA94516.1	AP001800	Oryza sativa	Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAB07906.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.14.
BAA94517.1	AP001800	Oryza sativa	Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAB07905.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.13.
AAA33915.1	L27821	Oryza sativa	receptor type serine/threonine kinase. protein kinase.
BAB18292.1	AP002860	Oryza sativa	putative receptor-like protein kinase. P0409B08.19.
BAA94529.2	AP001800	Oryza sativa	Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
SEQ ID NO: 499			
AAC36318.1	AF053127	Malus x domestica	leucine-rich receptor-like protein kinase. LRPKml.
AAF91324.1	AF244890	Glycine max	receptor-like protein kinase 3. RLK3. GmRLK3.

AAF91323.1	AF244889	Glycine max receptor-like protein kinase 2. RLK2. GmRLK2.
CAA61510.1	X89226	Oryza sativa leucine-rich repeat/receptor protein kinase. lrk2.
AAF59906.1	AF197947	Glycine max receptor protein kinase-like protein. CLV1B.
AAF59905.1	AF197946	Glycine max receptor protein kinase-like protein. CLV1A.
AAF91322.1	AF244888	Glycine max receptor-like protein kinase 1. RLK1. GmRLK1.
BAB40094.1	AP003210	Oryza sativa putative receptor protein kinase. OSJNBa0010K01.7.
CAC20842.1	AJ250467	Pinus sylvestris receptor protein kinase. upk.
AAB36558.1	U77888	Ipomoea nil receptor-like protein kinase INRPK1. inrpk1. leucine-rich repeat.
BAA83373.1	AP000391	Oryza sativa ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).
BAA84787.1	AP000559	Oryza sativa ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).
AAK27806.1	AC022457	Oryza sativa putative protein kinase. OSJNBa0006L06.21.
AAF34426.1	AF172282	Oryza sativa leucine rich repeat containing protein kinase. DUPR11.16.
BAB03627.1	AP002522	Oryza sativa putative protein kinase Xa21. P0009G03.27.
BAB03631.1	AP002522	Oryza sativa putative protein kinase Xa21. P0009G03.32.
AAK27817.1	AC022457	Oryza sativa putative protein kinase. OSJNBa0006L06.16.
BAB03621.1	AP002522	Oryza sativa putative protein kinase Xa21. P0009G03.21.
BAB03629.1	AP002522	Oryza sativa putative protein kinase Xa21. P0009G03.30.
AAC80225.1	U72723	Oryza longistaminata receptor kinase-like protein. Xa21. disease resistance gene.
AAC49123.1	U37133	Oryza sativa receptor kinase-like protein. Xa21. Xa21 disease resistance gene.
BAA82393.1	AP000367	Oryza sativa EST C96716(C10608) corresponds to a region of the predicted gene.; Similar to putative receptor protein kinase. (AC002334).

AAB82755.1	U72725	Oryza longistaminata	receptor kinase-like protein. Xa21 gene family member A1; downstream of microsatellite region; disease resistance gene family member.
AAG52992.1	U77888	Ipomoea nil	receptor-like protein kinase INRPK1a. inrpk1.
AAB82756.1	U72724	Oryza sativa	receptor kinase-like protein. Xa21 gene family member E.
AAB82753.1	U72726	Oryza longistaminata	receptor kinase-like protein. Xa21 gene family member D.
CAB51480.1	Y14600	Sorghum bicolor	putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.
BAA88636.1	AB029327	Nicotiana tabacum	elicitor-inducible LRR receptor-like protein EILP. EILP.
AAG52994.1	U77888	Ipomoea nil	receptor-like protein kinase INRPK1c. inrpk1.
BAA94519.1	AP001800	Oryza sativa	ESTs AU032341(R3918),AU071016(R10613) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 4, BAC F9D16; putative receptor kinase (AL035394).
BAB07903.1	AP002835	Oryza sativa	putative receptor kinase. P0417G05.10. contains ESTs AU032341(R3918),AU071016(R10613).
BAA87853.1	AP000816	Oryza sativa	EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
AAD38286.1	AC007789	Oryza sativa	putative protein kinase. OSJNBa0049B20.13.
BAB40081.1	AP003074	Oryza sativa	putative receptor protein kinase. OSJNBa0004G10.30.
BAB18321.1	AP002865	Oryza sativa	putative receptor protein kinase. P0034C11.11.
SEQ ID NO: 500			
BAB40094.1	AP003210	Oryza sativa	putative receptor protein kinase. OSJNBa0010K01.7.
AAC36318.1	AF053127	Malus x domestica	leucine-rich receptor-like protein kinase. LRPKml.
AAF59906.1	AF197947	Glycine max	receptor protein kinase-like protein. CLV1B.
AAF59905.1	AF197946	Glycine max	receptor protein kinase-like protein. CLV1A.
AAF91323.1	AF244889	Glycine max	receptor-like protein kinase 2. RLK2. GmRLK2.

AAF91322.1	AF244888	Glycine max receptor-like protein kinase 1. RLK1. GmRLK1.
AAF91324.1	AF244890	Glycine max receptor-like protein kinase 3. RLK3. GmRLK3.
CAA61510.1	X89226	Oryza sativa leucine-rich repeat/receptor protein kinase. lrk2.
CAC20842.1	AJ250467	Pinus sylvestris receptor protein kinase. upk.
BAA84787.1	AP000559	Oryza sativa ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).
BAA83373.1	AP000391	Oryza sativa ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).
AAK27806.1	AC022457	Oryza sativa putative protein kinase. OSJNBa0006L06.21.
AAB36558.1	U77888	Ipomoea nil receptor-like protein kinase INRPK1. inrpk1. leucine-rich repeat.
BAB03627.1	AP002522	Oryza sativa putative protein kinase Xa21. P0009G03.27.
BAB03629.1	AP002522	Oryza sativa putative protein kinase Xa21. P0009G03.30.
BAB03631.1	AP002522	Oryza sativa putative protein kinase Xa21. P0009G03.32.
BAB03621.1	AP002522	Oryza sativa putative protein kinase Xa21. P0009G03.21.
AAK27817.1	AC022457	Oryza sativa putative protein kinase. OSJNBa0006L06.16.
AAF34426.1	AF172282	Oryza sativa leucine rich repeat containing protein kinase. DUPR11.16.
AAB82755.1	U72725	Oryza longistaminata receptor kinase-like protein. Xa21 gene family member A1; downstream of microsatellite region; disease resistance gene family member.
AAC80225.1	U72723	Oryza longistaminata receptor kinase-like protein. Xa21. disease resistance gene.
AAC49123.1	U37133	Oryza sativa receptor kinase-like protein. Xa21. Xa21 disease resistance gene.
BAA82393.1	AP000367	Oryza sativa EST C96716(C10608) corresponds to a region of the predicted gene.; Similar to putative receptor protein kinase. (AC002334).
AAB82756.1	U72724	Oryza sativa receptor kinase-like protein. Xa21 gene family member E.

BAA88636.1 AB029327 *Nicotiana tabacum*
elicitor-inducible LRR receptor-like protein EILP. EILP.

AAG52992.1 U77888 *Ipomoea nil*
receptor-like protein kinase INRPK1a. inrpkl.

AAB82753.1 U72726 *Oryza longistaminata*
receptor kinase-like protein. Xa21 gene family member D.

CAB51480.1 Y14600 *Sorghum bicolor*
putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.

AAB61708.1 U93048 *Daucus carota*
somatic embryogenesis receptor-like kinase. SERK.

SEQ ID NO: 501

CAA73134.1 Y12531 *Brassica oleracea*
serine/threonine kinase. BRLK.

AAB93834.1 U82481 *Zea mays*
KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.

CAA67145.1 X98520 *Brassica oleracea*
receptor-like kinase. SFR2.

CAA73133.1 Y12530 *Brassica oleracea*
serine /threonine kinase. ARLK.

CAA74661.1 Y14285 *Brassica oleracea*
SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.

AAA62232.1 U00443 *Brassica napus*
S-receptor kinase. protein contains an immunoglobulin-like domain.

BAA92836.1 AB032473 *Brassica oleracea*
S18 S-locus receptor kinase. SRK18.

CAB41878.1 Y18259 *Brassica oleracea*
SRK5 protein. SRK5. receptor-like kinase.

AAC23542.1 U20948 *Ipomoea trifida*
receptor protein kinase. IRK1.

BAA23676.1 AB000970 *Brassica rapa*
receptor kinase 1. BcRK1.

CAB41879.1 Y18260 *Brassica oleracea*
SRK15 protein. SRK15. receptor-like kinase.

AAA33000.1 M76647 *Brassica oleracea*
receptor protein kinase. SKR6.

AAA33008.1 M97667 *Brassica napus*
serine/threonine kinase receptor.

CAB89179.1 AJ245479 *Brassica napus* subsp. *napus*
ser /thr kinase. S-locus receptor kinase. srk.

CAA74662.1 Y14286 *Brassica oleracea*
SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.

BAA06285.1 D30049 *Brassica rapa*
S-receptor kinase SRK9.

BAA21132.1 D88193 *Brassica rapa*
S-receptor kinase. SRK9 (B.c).

BAA07577.2 D38564 *Brassica rapa*
receptor protein kinase SRK12.

CAA79355.1 Z18921 *Brassica oleracea*
S-receptor kinase-like protein.

BAA07576.1 D38563 *Brassica rapa*
receptor protein kinase SRK8.

BAB21001.1 AB054061 *Brassica rapa*
S locus receptor kinase. SRK22.

BAA92837.1 AB032474 *Brassica oleracea*
S60 S-locus receptor kinase. SRK60.

AAD21872.1 AF078082 *Phaseolus vulgaris*
receptor-like protein kinase homolog RK20-1.

AAF34428.1 AF172282 *Oryza sativa*
receptor-like protein kinase. DUPR11.18.

AAD52097.1 AF088885 *Nicotiana tabacum*
receptor-like kinase CHRK1. Chrkl.

BAB07906.1 AP002835 *Oryza sativa*
putative S-receptor kinase. P0417G05.14.

BAA94516.1 AP001800 *Oryza sativa*
Similar to *Zea mays* S-domain receptor-like protein kinase (AJ010166).

BAB18292.1 AP002860 *Oryza sativa*
putative receptor-like protein kinase. P0409B08.19.

BAB07904.1 AP002835 *Oryza sativa*
putative S-receptor kinase. P0417G05.12.

BAA94518.1 AP001800 *Oryza sativa*
Similar to *Arabidopsis thaliana* chromosome 2 section 111 of 255; putative receptor-like protein kinase (AC002392).

SEQ ID NO: 502

AAC78596.1 AF053998 *Lycopersicon esculentum*
Hcr2-5D. Hcr2-5D. similar to *Lycopersicon pimpinellifolium* disease resistance protein Cf-2.2 encoded by the sequence presented in GenBank Accession Number U42445.

AAC78591.1 AF053993 *Lycopersicon esculentum*
disease resistance protein. Cf-5.

AAC78593.1 AF053995 *Lycopersicon esculentum*
Hcr2-0B. Hcr2-0B. similar to *Lycopersicon pimpinellifolium* disease resistance protein Cf-2.2 encoded by the sequence presented in GenBank Accession Number U42445.

AAC78592.1 AF053994 *Lycopersicon esculentum*
Hcr2-0A. Hcr2-0A. similar to *Lycopersicon pimpinellifolium* disease resistance protein Cf-2.2 encoded by the sequence presented in GenBank Accession Number U42445.

AAC78594.1 AF053996 *Lycopersicon pimpinellifolium*
Hcr2-2A. Hcr2-2A. similar to *Lycopersicon pimpinellifolium* disease resistance protein Cf-2.2 encoded by the sequence presented in GenBank Accession Number U42445.

CAA05274.1 AJ002236 *Lycopersicon pimpinellifolium*
resistance gene. Cf-9. Cf-9.

AAA65235.1 U15936 *Lycopersicon pimpinellifolium*
Cf-9 precursor. Cf-9. this is the ninth resistance gene to disease caused by *Cladosporium fulvum* to be isolated.

CAA05276.1 AJ002236 *Lycopersicon pimpinellifolium*
resistance gene. Hcr9-9E. Hcr9-9E.

AAC78595.1 AF053997 *Lycopersicon esculentum*
Hcr2-5B. Hcr2-5B. similar to *Lycopersicon pimpinellifolium* disease resistance protein Cf-2.2 encoded by the sequence presented in GenBank Accession Number U42445.

CAA05268.1 AJ002235 *Lycopersicon hirsutum*
Resistance gene. Cf-4. Cf-4.

CAA05279.1 AJ002237 *Lycopersicon esculentum*
Hcr9-0. Hcr9-0. homologue of *Cladosporium fulvum* disease resistance gene Cf-9.

BAB08215.1 AP002539 *Oryza sativa*
Similar to *Lycopersicon esculentum* disease resistance protein (AF053993).

BAA96776.1 AP002521 *Oryza sativa*
Similar to *Lycopersicon esculentum* disease resistance protein (AF053993).

AAG21897.1 AC026815 *Oryza sativa*
putative disease resistance protein (3' partial). OSJNBa0079L16.21.

AAD50430.1 AF166121 *Hordeum vulgare*
Cf2/Cf5 disease resistance protein homolog. Big1. leucine rich repeat protein.

AAG21917.1 AC026815 *Oryza sativa*
putative disease resistance protein. OSJNBa0079L16.5.

CAB55409.1 AL117265 *Oryza sativa*
zhb0001.1. Incomplete at 5'end, Similar to disease resistance protein; Method: conceptual translation with partial peptide sequencing.

AAG21909.1 AC026815 *Oryza sativa*
putative disease resistance protein. OSJNBa0079L16.3.

AAC80225.1 U72723 *Oryza longistaminata*
receptor kinase-like protein. Xa21. disease resistance gene.

AAC49123.1 U37133 *Oryza sativa*
receptor kinase-like protein. Xa21. Xa21 disease resistance gene.

SEQ ID NO: 503

CAA05276.1 AJ002236 *Lycopersicon pimpinellifolium*
resistance gene. Hcr9-9E. Hcr9-9E.

AAC78592.1	AF053994	<i>Lycopersicon esculentum</i> Hcr2-0A. Hcr2-0A. similar to <i>Lycopersicon pimpinellifolium</i> disease resistance protein Cf-2.2 encoded by the sequence presented in GenBank Accession Number U42445.
CAA05274.1	AJ002236	<i>Lycopersicon pimpinellifolium</i> resistance gene. Cf-9. Cf-9.
AAA65235.1	U15936	<i>Lycopersicon pimpinellifolium</i> Cf-9 precursor. Cf-9. this is the ninth resistance gene to disease caused by <i>Cladosporium fulvum</i> to be isolated.
AAC78594.1	AF053996	<i>Lycopersicon pimpinellifolium</i> Hcr2-2A. Hcr2-2A. similar to <i>Lycopersicon pimpinellifolium</i> disease resistance protein Cf-2.2 encoded by the sequence presented in GenBank Accession Number U42445.
CAA05279.1	AJ002237	<i>Lycopersicon esculentum</i> Hcr9-0. Hcr9-0. homologue of <i>Cladosporium fulvum</i> disease resistance gene Cf-9.
AAC78595.1	AF053997	<i>Lycopersicon esculentum</i> Hcr2-5B. Hcr2-5B. similar to <i>Lycopersicon pimpinellifolium</i> disease resistance protein Cf-2.2 encoded by the sequence presented in GenBank Accession Number U42445.
AAC78593.1	AF053995	<i>Lycopersicon esculentum</i> Hcr2-0B. Hcr2-0B. similar to <i>Lycopersicon pimpinellifolium</i> disease resistance protein Cf-2.2 encoded by the sequence presented in GenBank Accession Number U42445.
CAA05268.1	AJ002235	<i>Lycopersicon hirsutum</i> Resistance gene. Cf-4. Cf-4.
AAC78596.1	AF053998	<i>Lycopersicon esculentum</i> Hcr2-5D. Hcr2-5D. similar to <i>Lycopersicon pimpinellifolium</i> disease resistance protein Cf-2.2 encoded by the sequence presented in GenBank Accession Number U42445.
AAC78591.1	AF053993	<i>Lycopersicon esculentum</i> disease resistance protein. Cf-5.
BAA96776.1	AP002521	<i>Oryza sativa</i> Similar to <i>Lycopersicon esculentum</i> disease resistance protein (AF053993).
BAB08215.1	AP002539	<i>Oryza sativa</i> Similar to <i>Lycopersicon esculentum</i> disease resistance protein (AF053993).
CAB55409.1	AL117265	<i>Oryza sativa</i> zhb0001.1. Incomplete at 5'end, Similar to disease resistance protein; Method: conceptual translation with partial peptide sequencing.
AAD50430.1	AF166121	<i>Hordeum vulgare</i> Cf2/Cf5 disease resistance protein homolog. Big1. leucine rich repeat protein.
AAG21897.1	AC026815	<i>Oryza sativa</i> putative disease resistance protein (3' partial). OSJNBa0079L16.21.
AAB82755.1	U72725	<i>Oryza longistaminata</i> receptor kinase-like protein. Xa21 gene family member A1; downstream of microsatellite region; disease resistance gene family member.
SEQ ID NO: 504		
AAF91324.1	AF244890	<i>Glycine max</i> receptor-like protein kinase 3. RLK3. GmRLK3.

BAA84787.1	AP000559	Oryza sativa	ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).
BAA83373.1	AP000391	Oryza sativa	ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).
AAF91322.1	AF244888	Glycine max	receptor-like protein kinase 1. RLK1. GmRLK1.
AAF91323.1	AF244889	Glycine max	receptor-like protein kinase 2. RLK2. GmRLK2.
CAC20842.1	AJ250467	Pinus sylvestris	receptor protein kinase. upk.
AAK27806.1	AC022457	Oryza sativa	putative protein kinase. OSJNBa0006L06.21.
AAB36558.1	U77888	Ipomoea nil	receptor-like protein kinase INRPK1. inrpk1. leucine-rich repeat.
BAA82393.1	AP000367	Oryza sativa	EST C96716(C10608) corresponds to a region of the predicted gene.; Similar to putative receptor protein kinase. (AC002334).
AAF59906.1	AF197947	Glycine max	receptor protein kinase-like protein. CLV1B.
BAB03629.1	AP002522	Oryza sativa	putative protein kinase Xa21. P0009G03.30.
BAB03627.1	AP002522	Oryza sativa	putative protein kinase Xa21. P0009G03.27.
AAF59905.1	AF197946	Glycine max	receptor protein kinase-like protein. CLV1A.
AAK27817.1	AC022457	Oryza sativa	putative protein kinase. OSJNBa0006L06.16.
BAB03631.1	AP002522	Oryza sativa	putative protein kinase Xa21. P0009G03.32.
BAB03621.1	AP002522	Oryza sativa	putative protein kinase Xa21. P0009G03.21.
AAF34426.1	AF172282	Oryza sativa	leucine rich repeat containing protein kinase. DUPR11.16.
AAF66615.1	AF142596	Nicotiana tabacum	LRR receptor-like protein kinase.
AAB82755.1	U72725	Oryza longistaminata	receptor kinase-like protein. Xa21 gene family member A1; downstream of microsatellite region; disease resistance gene family member.
AAC49123.1	U37133	Oryza sativa	receptor kinase-like protein. Xa21. Xa21 disease resistance gene.

AAC80225.1	U72723	<i>Oryza longistaminata</i> receptor kinase-like protein. Xa21. disease resistance gene.
BAB19337.1	AP003044	<i>Oryza sativa</i> putative protein kinase. P0038C05.10. contains ESTs AU056335(S20481),AU056336(S20481).
BAA88636.1	AB029327	<i>Nicotiana tabacum</i> elicitor-inducible LRR receptor-like protein EILP. EILP.
CAB51480.1	Y14600	<i>Sorghum bicolor</i> putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.
AAK21965.1	AY028699	<i>Brassica napus</i> receptor protein kinase PERK1.
BAB39409.1	AP002901	<i>Oryza sativa</i> putative protein kinase. P0456F08.9. contains EST C23560(R0290).
BAB07903.1	AP002835	<i>Oryza sativa</i> putative receptor kinase. P0417G05.10. contains ESTs AU032341(R3918),AU071016(R10613).
BAA94519.1	AP001800	<i>Oryza sativa</i> ESTs AU032341(R3918),AU071016(R10613) correspond to a region of the predicted gene. Similar to <i>Arabidopsis thaliana</i> chromosome 4, BAC F9D16; putative receptor kinase (AL035394).
AAK00425.1	AC069324	<i>Oryza sativa</i> Putative protein kinase. OSJNBa0071K19.11.
AAG59657.1	AC084319	<i>Oryza sativa</i> putative protein kinase. OSJNBa0004B24.20.
BAA87853.1	AP000816	<i>Oryza sativa</i> EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
BAB39873.1	AP002882	<i>Oryza sativa</i> putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
AAB82756.1	U72724	<i>Oryza sativa</i> receptor kinase-like protein. Xa21 gene family member E.
AAB82753.1	U72726	<i>Oryza longistaminata</i> receptor kinase-like protein. Xa21 gene family member D.
SEQ ID NO: 505		
CAA73134.1	Y12531	<i>Brassica oleracea</i> serine/threonine kinase. BRLK.
CAA74661.1	Y14285	<i>Brassica oleracea</i> SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.
AAC23542.1	U20948	<i>Ipomoea trifida</i> receptor protein kinase. IRK1.

BAA23676.1	AB000970	Brassica rapa	receptor kinase 1. BcRK1.
AAB93834.1	U82481	Zea mays	KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
CAA73133.1	Y12530	Brassica oleracea	serine /threonine kinase. ARLK.
CAA67145.1	X98520	Brassica oleracea	receptor-like kinase. SFR2.
CAB89179.1	AJ245479	Brassica napus subsp. napus	ser /thr kinase. S-locus receptor kinase. srk.
AAA33008.1	M97667	Brassica napus	serine/threonine kinase receptor.
BAA21132.1	D88193	Brassica rapa	S-receptor kinase. SRK9 (B.c).
AAA62232.1	U00443	Brassica napus	S-receptor kinase. protein contains an immunoglobulin-like domain.
BAA06285.1	D30049	Brassica rapa	S-receptor kinase SRK9.
CAA74662.1	Y14286	Brassica oleracea	SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
AAA33000.1	M76647	Brassica oleracea	receptor protein kinase. SKR6.
BAA07576.1	D38563	Brassica rapa	receptor protein kinase SRK8.
BAA92836.1	AB032473	Brassica oleracea	S18 S-locus receptor kinase. SRK18.
CAB41878.1	Y18259	Brassica oleracea	SRK5 protein. SRK5. receptor-like kinase.
CAA79355.1	Z18921	Brassica oleracea	S-receptor kinase-like protein.
CAB41879.1	Y18260	Brassica oleracea	SRK15 protein. SRK15. receptor-like kinase.
BAB21001.1	AB054061	Brassica rapa	S locus receptor kinase. SRK22.
BAA92837.1	AB032474	Brassica oleracea	S60 S-locus receptor kinase. SRK60.
BAA07577.2	D38564	Brassica rapa	receptor protein kinase SRK12.
AAD21872.1	AF078082	Phaseolus vulgaris	receptor-like protein kinase homolog RK20-1.

BAA94517.1	AP001800	Oryza sativa	Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAB07905.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.13.
BAB07906.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.14.
BAA94516.1	AP001800	Oryza sativa	Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
AAD52097.1	AF088885	Nicotiana tabacum	receptor-like kinase CHRK1. Chrkl.
BAB18292.1	AP002860	Oryza sativa	putative receptor-like protein kinase. P0409B08.19.
SEQ ID NO: 507			
AAA33509.1	M62985	Zea mays	protein kinase. putative; putative.
CAA62476.1	X90990	Solanum tuberosum	stpk1 protein kinase.
AAK31277.1	AC079890	Oryza sativa	putative protein kinase. OSJNBb0089A17.15.
CAA66616.1	X97980	Solanum berthaultii	protein kinase.
AAF66637.1	AF143505	Lycopersicon esculentum	viroid symptom modulation protein. PKv. protein kinase; induced by viroid infection.
BAA96593.1	AP002481	Oryza sativa	Similar to Solanum berthaultii protein kinase. (X97980).
AAB54117.1	U93559	Brassica rapa	putative serine/threonine protein kinase. Bcpk1.
AAB88817.1	AF033263	Zea mays	signal transduction for phototropism. nonphototropic hypocotyl 1. nph1. NPH1; putative serine/threonine kinase; similar to oat NPH1 proteins.
AAC05084.1	AF033097	Avena sativa	NPH1-2. NPH1-2. putative serine/threonine protein kinase.
CAA82994.1	Z30333	Mesembryanthemum crystallinum	protein kinase.
AAC05083.1	AF033096	Avena sativa	NPH1-1. NPH1-1. putative serine/threonine protein kinase.
CAA82992.1	Z30331	Mesembryanthemum crystallinum	Protein Kinase.
CAA82993.1	Z30332	Spinacia oleracea	protein kinase.
AAA50304.1	M92989	Pisum sativum	protein kinase. PK5. homologue.

AAB71418.1	U11553	Pisum sativum	PsPK3. putative protein kinase.
BAA93704.1	AB032564	Cucumis sativus	cucumber protein kinase CsPK3. CsPK3. putative.
BAA36192.1	AB012082	Adiantum capillus-veneris	PHY3. PHY3. Ser/Thr protein kinase; chimeric structure of red/far-red light photoreceptive region (phytochrome) and putative blue light photoreceptor in phototropism of hypocotyl (NPH1).
AAK18843.1	AC082645	Oryza sativa	putative protein kinase. OSJNBb0033N16.3.
CAB82852.1	Z30329	Mesembryanthemum crystallinum	protein kinase MK6.
CAA50374.1	X71057	Nicotiana tabacum	protein kinase. PKTL7.
AAK13156.1	AC078829	Oryza sativa	putative protein kinase. OSJNBa0026O12.14.
BAB03409.1	AP002816	Oryza sativa	Similar to Spinacia oleracea protein kinase (S42867).
CAA82991.1	Z30330	Spinacia oleracea	protein kinase.
AAD50584.1	AF089097	Salvia columbariae	protein kinase 1. PK1.
AAB93860.1	U89679	Lycopersicon esculentum	protein kinase. LePK2. contains catalytic domain.
AAD50585.1	AF089099	Salvia columbariae	protein kinase 3. PK3.
AAD50586.1	AF089100	Salvia columbariae	protein kinase 4. PK4.
AAB93859.1	U89678	Lycopersicon esculentum	protein kinase. LePK1. contains catalytic domain.
AAA50772.1	M69030	Pisum sativum	protein serine/threonine kinase. PsPK1. putative; putative.
AAB93861.1	U89680	Lycopersicon esculentum	protein kinase. LePK3. contains catalytic domain.
AAD50587.1	AF089101	Salvia columbariae	protein kinase 5. PK5.
AAD50588.1	AF089102	Salvia columbariae	protein kinase 6. PK6.
CAA56313.1	X79992	Avena sativa	putative pp70 ribosomal protein S6 kinase. Aspkl1.
AAD50589.1	AF089103	Salvia columbariae	protein kinase 7. PK7.

CAB89082.1 AJ277534 *Asparagus officinalis*

S6 ribosomal protein kinase. pk1. putative.

AAB93862.1 U89681 *Lycopersicon esculentum*

protein kinase. LePK4. contains catalytic domain.

BAA92972.1 AP001551 *Oryza sativa*

ESTs AU056183(S20356), AU056881(S20950) correspond to a region of the predicted gene. Similar to *Arabidopsis thaliana* chromosome 4 BAC clone F6I18 ; putative protein kinase. (AL022198).

BAB12687.1 AP002746 *Oryza sativa*

putative protein kinase. P0671B11.2. contains ESTs C22394(C30013), C22393(C30013).

SEQ ID NO: 508

BAA23676.1 AB000970 *Brassica rapa*

receptor kinase 1. BcRK1.

CAA74662.1 Y14286 *Brassica oleracea*

SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.

CAA74661.1 Y14285 *Brassica oleracea*

SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.

CAA73133.1 Y12530 *Brassica oleracea*

serine /threonine kinase. ARLK.

CAA67145.1 X98520 *Brassica oleracea*

receptor-like kinase. SFR2.

AAA33008.1 M97667 *Brassica napus*

serine/threonine kinase receptor.

CAB89179.1 AJ245479 *Brassica napus* subsp. *napus*

ser /thr kinase. S-locus receptor kinase. srk.

CAA79355.1 Z18921 *Brassica oleracea*

S-receptor kinase-like protein.

CAB41878.1 Y18259 *Brassica oleracea*

SRK5 protein. SRK5. receptor-like kinase.

AAA33000.1 M76647 *Brassica oleracea*

receptor protein kinase. SKR6.

BAA92837.1 AB032474 *Brassica oleracea*

S60 S-locus receptor kinase. SRK60.

BAA21132.1 D88193 *Brassica rapa*

S-receptor kinase. SRK9 (B.c).

BAA06285.1 D30049 *Brassica rapa*

S-receptor kinase SRK9.

AAA62232.1 U00443 *Brassica napus*

S-receptor kinase. protein contains an immunoglobulin-like domain.

BAA92836.1 AB032473 *Brassica oleracea*

S18 S-locus receptor kinase. SRK18.

BAB21001.1	AB054061	Brassica rapa	S locus receptor kinase. SRK22.
BAA07576.1	D38563	Brassica rapa	receptor protein kinase SRK8.
BAA07577.2	D38564	Brassica rapa	receptor protein kinase SRK12.
CAA73134.1	Y12531	Brassica oleracea	serine/threonine kinase. BRLK.
AAB93834.1	U82481	Zea mays	KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
AAC23542.1	U20948	Ipomoea trifida	receptor protein kinase. IRK1.
CAB41879.1	Y18260	Brassica oleracea	SRK15 protein. SRK15. receptor-like kinase.
AAD52097.1	AF088885	Nicotiana tabacum	receptor-like kinase CHRK1. Chrk1.
AAD21872.1	AF078082	Phaseolus vulgaris	receptor-like protein kinase homolog RK20-1.
BAB18292.1	AP002860	Oryza sativa	putative receptor-like protein kinase. P0409B08.19.
AAK02023.1	AC074283	Oryza sativa	Putative protein kinase-like. OSJNBa0087H07.5.
CAA79324.1	Z18884	Brassica oleracea	S-receptor kinase related protein.
BAB21240.1	AP002953	Oryza sativa	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
CAB51836.1	AJ243961	Oryza sativa	Putative Ser/Thr protein kinase. 11332.7.
AAK21965.1	AY028699	Brassica napus	receptor protein kinase PERK1.
BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
BAA94509.1	AB041503	Populus nigra	protein kinase 1. PnPK1.
AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.
BAA94510.1	AB041504	Populus nigra	protein kinase 2. PnPK2.
BAA92953.1	AP001551	Oryza sativa	Similar to Arabidopsis thaliana chromosome 4 BAC clone F10M6 ; S-receptor kinase -like protein. (AL021811).

BAA92954.1 AP001551 *Oryza sativa*
Similar to *Oryza sativa* protein kinase (OSPK10) mRNA. (L27821).
AAG16628.1 AY007545 *Brassica napus*
protein serine/threonine kinase BNK1.
BAB16871.1 AP002537 *Oryza sativa*
putative protein kinase APK1A *Arabidopsis thaliana*. P0001B06.24. contains ESTs
C22608(R3192), D25110(R3192).

SEQ ID NO: 510

AAG30254.1 AF307333 *Hordeum vulgare*
putative nematode-resistance protein. Hs1. similar to *Beta procumbens* Hs1pro protein.
AAB48305.1 U79733 *Beta procumbens*
nematode resistance. Hs1pro-1.

SEQ ID NO: 513

BAA14144.1 D90116 *Armoracia rusticana*
peroxidase isozyme.
BAA14143.1 D90115 *Armoracia rusticana*
peroxidase isozyme.
BAA11853.1 D83225 *Populus nigra*
peroxidase.
CAA66037.1 X97351 *Populus balsamifera* subsp. *trichocarpa*
signal for ER. peroxidase.
CAA66034.1 X97348 *Populus balsamifera* subsp. *trichocarpa*
signal for ER. peroxidase.
CAA66036.1 X97350 *Populus balsamifera* subsp. *trichocarpa*
signal for ER. peroxidase.
CAA66035.1 X97349 *Populus balsamifera* subsp. *trichocarpa*
signal for ER. peroxidase.
BAA11852.1 D83224 *Populus nigra*
peroxidase.
BAA07241.1 D38051 *Populus kitakamiensis*
peroxidase. prxA4a.
BAA06335.1 D30653 *Populus kitakamiensis*
peroxidase.
AAB47602.1 L07554 *Linum usitatissimum*
peroxidase. FLXPER1.
AAC98519.1 AF007211 *Glycine max*
peroxidase precursor. GMIPER1. pathogen-induced.
AAD37427.1 AF149277 *Phaseolus vulgaris*
peroxidase 1 precursor. FBP1. secretory peroxidase.
BAA06334.1 D30652 *Populus kitakamiensis*
peroxidase.
AAB97734.1 AF014502 *Glycine max*
seed coat peroxidase precursor. Ep. H₂O₂ oxidoreductase; class III plant peroxidase.

CAB94692.1	AJ242742	<i>Ipomoea batatas</i>	Removal of H ₂ O ₂ , oxidation of toxic reductants, defence response toward wounding. peroxidase. pod.
CAA62227.1	X90694	<i>Medicago sativa</i>	peroxidase1C. prx1C.
CAA62226.1	X90693	<i>Medicago sativa</i>	peroxidase1B. prx1B.
AAD37430.1	AF149280	<i>Phaseolus vulgaris</i>	peroxidase 5 precursor. FBP5. secretory peroxidase.
CAA62225.1	X90692	<i>Medicago sativa</i>	peroxidase1A. prx1A.
AAB41811.1	L36157	<i>Medicago sativa</i>	peroxidase. pxdC. amino acid feature: conserved domains, aa 123 .. 129, 191 .. 198; amino acid feature: heme-binding domain, aa 68 .. 73.
AAB41810.1	L36156	<i>Medicago sativa</i>	peroxidase. pxdA. amino acid feature: conserved motifs, aa 181 .. 188; amino acid feature: heme-binding domain, aa 60 .. 65.
BAA01877.1	D11102	<i>Populus kitakamiensis</i>	peroxidase. prxA1.
CAB67121.1	Y19023	<i>Lycopersicon esculentum</i>	peroxidase. cevi-1.
CAA50597.1	X71593	<i>Lycopersicon esculentum</i>	peroxidase. CEVI-1.
BAA01992.1	D11396	<i>Nicotiana tabacum</i>	'peroxidase'.
AAA34108.1	J02979	<i>Nicotiana tabacum</i>	lignin-forming peroxidase precursor (EC 1.11.1.7).
AAA33127.1	M91373	<i>Cucumis sativus</i>	peroxidase. pre-peroxidase. putative.
BAA92500.1	AP001383	<i>Oryza sativa</i>	ESTs D39300(R3292), AU030751(E60187) correspond to a region of the predicted gene. Similar to peroxidase ATP6a. (X98774).
CAB65334.1	AJ250121	<i>Picea abies</i>	peroxidase. SPI2 protein. spi2.
CAA40796.1	X57564	<i>Armoracia rusticana</i>	peroxidase. peroxidase precursor.
AAB06183.1	M37636	<i>Arachis hypogaea</i>	cationic peroxidase. PNC1.
CAA76680.1	Y17192	<i>Cucurbita pepo</i>	peroxidase. aprx. type III peroxidase.
AAA33129.1	M91372	<i>Cucumis sativus</i>	peroxidase. pre-peroxidase.

CAA71492.1	Y10466	Spinacia oleracea	peroxidase. prxr5.
AAF63027.1	AF244924	Spinacia oleracea	hydrogen peroxide catabolism. peroxidase prx15 precursor. type III peroxidase.
AAD43561.1	AF155124	Gossypium hirsutum	bacterial-induced peroxidase precursor. Perx_Goshiko.
AAF63026.1	AF244923	Spinacia oleracea	hydrogen peroxide catabolism. peroxidase prx14 precursor. type III peroxidase.
AAA33121.1	M32742	Cucumis sativus	peroxidase (CuPer2).
BAA92422.1	AP001366	Oryza sativa	ESTs AU081576(R0541),AU032412(R4029) correspond to a region of the predicted gene. Similar to A.thaliana mRNA for peroxidase ATP18a. (X98804).
BAA92497.1	AP001383	Oryza sativa	ESTs AU081576(R0541),AU032412(R4029) correspond to a region of the predicted gene. Similar to peroxidase ATP18a. (X98804).
BAA77389.1	AB024439	Scutellaria baicalensis	peroxidase 3.
BAA08499.1	D49551	Oryza sativa	peroxidase. poxN.
AAB19129.1	U41657	Glycine max	seed coat peroxidase isozyme. SPOD4.1. H2O2 oxidoreductase.
BAA03373.1	D14482	Oryza sativa	putative peroxidase.
AAB02554.1	L37790	Stylosanthes humilis	cationic peroxidase.
SEQ ID NO: 515			
AAB88134.1	AF034618	Spinacia oleracea	cytosolic heat shock 70 protein. HSC70-1.
AAF34134.1	AF161180	Malus x domestica	high molecular weight heat shock protein. Hsp2.
AAB99745.1	AF005993	Triticum aestivum	HSP70. TaHSP70d. 70 kDa heat shock protein, molecular chaperone.
AAA62325.1	L32165	Hordeum vulgare	Molecular chaperone. HSP70. Heat-shock protein HSP70; The predicted amino acid sequence is highly homologous (more than 80% identity) to other plant heat-shock proteins (HSP70s) in the database; however the C terminus is quite unique.; putative.
AAA21808.1	L23551	Spinacia oleracea	molecular chaperone. ER-lumenal protein. HSC70.
AAA34139.1	L08830	Lycopersicon esculentum	molecular chaperon (precursor). glucose-regulated protein 78. BiP/grp78. an endoplasmic reticulum residing heat shock protein 70 family member; precursor peptide.

AAB86942.1 AF031241 Glycine max
endoplasmic reticulum transport protein; molecular chaperone; roles in protein folding,
assembly, and transport. endoplasmic reticulum HSC70-cognate binding protein precursor.
BiP. BiP; similar to HSC70 and GRP78.

AAK21920.1 AF338252 Glycine max
molecular chaperone. BiP-isoform D. BiPD. ER-lumenal HSP70; binding protein GRP78.

AAB91473.1 AF035458 Spinacia oleracea
heat shock 70 protein. HSC70-11. mitochondrial protein.

AAB96660.1 AF039084 Spinacia oleracea
heat shock 70 protein. HSC70-11. molecular chaperone.

AAB91472.1 AF035457 Spinacia oleracea
heat shock 70 protein. HSC70-10. mitochondrial protein.

SEQ ID NO: 516

CAA06927.1 AJ006233 Nicotiana tabacum
putative thaumatin-like protein precursor.

AAF06346.1 AF195653 Vitis vinifera
SCUTL1. thaumatin-like protein.

BAA28872.1 AB006009 Pyrus pyrifolia
thaumatin-like protein precursor. PsTL1.

CAC10270.1 AJ243427 Malus x domestica
thaumatin-like protein. tl. allergen, pathogenesis-related.

AAC36740.1 AF090143 Malus x domestica
thaumatin-like protein precursor Mdtl1. MDTL1. pathogenesis-related.

CAB62167.1 AJ242828 Castanea sativa
antifungal. thaumatin-like protein. tl1.

AAB38064.1 U32440 Prunus avium
thaumatin-like protein precursor.

BAA74546.2 AB000834 Nicotiana tabacum
thaumatin-like protein SE39b.

AAF06347.1 AF195654 Vitis vinifera
SCUTL2. thaumatin-like protein.

CAC09477.1 AL442113 Oryza sativa
thaumatin-like protein. H0806H05.10.

AAB95118.1 U71244 Brassica rapa
pathogenesis-related group 5 protein. BFTP. thaumatin-like protein; PR-5.

CAA10492.1 AJ131731 Pseudotsuga menziesii
Thaumatin-like protein. 5A1A.16.

BAA95017.1 AB031870 Cestrum elegans
thaumatin-like protein. CETLP.

BAA95165.1 AB029918 Nicotiana tabacum
pistil transmitting tissue specific thaumatin (SE39b)-like protein. SE39b.

AAB61590.1 AF003007 Vitis vinifera
VVTL1. osmotin-like protein, PR-5 protein; thaumatin-like protein.

AAD55090.1 AF178653 *Vitis riparia*
thaumatin. osmotin; pathogenesis-related protein.

CAB85637.1 AJ237999 *Vitis vinifera*
putative thaumatin-like protein. T11. alternative name grip 51.

AAF82264.1 AF227324 *Vitis vinifera*
thaumatin-like protein.

AAB02259.1 U57787 *Avena sativa*
permatin precursor. thaumatin-like protein.

AAB53368.1 U77657 *Oryza sativa*
pathogenesis-related thaumatin-like protein.

CAA09228.1 AJ010501 *Cicer arietinum*
thaumatin-like protein PR-5b.

CAA33293.1 X15224 *Nicotiana tabacum*
thaumatin-like protein. E22.

CAA33292.1 X15223 *Nicotiana tabacum*
thaumatin-like protein. E2.

SEQ ID NO: 517

CAA71801.1 Y10848 *Brassica juncea*
gamma-glutamylcysteine synthetase. gsh1.

AAB71230.1 AF017983 *Lycopersicon esculentum*
gamma-glutamylcysteine synthetase. GSH1.

AAC82334.1 AF041340 *Medicago truncatula*
gamma-glutamylcysteine synthetase. putative plastid protein.

AAF22137.1 AF128455 *Pisum sativum*
gamma-glutamylcysteine synthetase precursor. gsh1. putative plastid protein.

AAF22136.1 AF128454 *Phaseolus vulgaris*
gamma-glutamylcysteine synthetase precursor. gsh1. putative plastid protein.

CAA06613.1 AJ005587 *Brassica juncea*
gamma-glutamylcysteine synthetase.

AAG13459.1 AF128453 *Glycine max*
gamma-glutamylcysteine synthetase precursor. gsh1.

CAA64808.1 X95563 *Brassica juncea*
gamma-glutamylcysteine synthetase. gsh1.

SEQ ID NO: 518

AAA75414.1 L28005 *Glycine max*
TGACG-motif-binding protein. STGA1.

AAB31250.2 S73827 *Solanum tuberosum*
mas-binding factor MBF3. transcription factor TGA1a homolog; This sequence comes from Fig. 4.

AAB31249.1 S73826 *Solanum tuberosum*
mas-binding factor MBF2. mas-binding factor MBF2. transcription factor TGA1a homolog; This sequence comes from Fig. 4.

CAA34468.1	X16449	Nicotiana sp.	TGA1a protein (AA 1-359).
AAA34091.1	M62855	Nicotiana tabacum	ASF-1/G13. leucine-zipper DNA-binding protein.
AAB31251.2	S73828	Solanum tuberosum	mas-binding factor MBF1. transcription factor TGA1a homolog; This sequence comes from Fig. 4.
CAA48904.1	X69152	Zea mays	ocs-element binding factor 3.2. OBF3.2.
CAA48905.1	X69153	Zea mays	ocs-element binding factor 3.1. OBF3.1.
AAC24123.1	AF067187	Cichorium intybus	cAMP responsive element binding protein. bZIP transcription factor; CREB.
AAC24122.1	AF067186	Cichorium intybus	cAMP responsive element binding protein. CREB1.
AAC49760.1	AF001454	Helianthus annuus	Dc3 promoter-binding factor-2. DPBF-2.
SEQ ID NO: 521			
CAA10608.1	AJ132228	Ricinus communis	amino acid carrier. aap3.
CAA07563.1	AJ007574	Ricinus communis	amino acid carrier. aap1.
CAA70778.1	Y09591	Vicia faba	amino acid transporter.
AAD16014.1	AF080543	Nepenthes alata	amino acid transporter. AAP2.
CAA70969.1	Y09826	Solanum tuberosum	amino acid transporter. AAP2. transmembrane protein.
AAD16015.1	AF080544	Nepenthes alata	amino acid transporter. AAP3.
CAA70968.1	Y09825	Solanum tuberosum	amino acid transporter. AAP1. transmembrane protein.
CAA92992.1	Z68759	Ricinus communis	amino acid carrier.
AAD16013.1	AF080542	Nepenthes alata	amino acid transporter. AAP1.
AAF15945.1	AF061435	Vicia faba	amino acid transporter b. AAPB.
CAA72006.1	Y11121	Ricinus communis	amino acid carrier.
AAF15944.1	AF061434	Vicia faba	amino acid transporter a. AAPA.

AAF15946.1 AF061436 *Vicia faba*
amino acid transporter c. AAPC.

AAB48944.1 U31932 *Nicotiana sylvestris*
amino acid permease 1. NSAAP1. amino acid transporter; Method: conceptual translation
supplied by author.

AAB96830.1 U64823 *Nicotiana sylvestris*
amino acid transporter. amino acid permease. nsaap1.

BAA93437.1 AB022783 *Oryza sativa*
amino acid permease. OsproT.

AAD25162.1 AF014810 *Lycopersicon esculentum*
proline transporter 3. LeProT3.

AAD25161.1 AF014809 *Lycopersicon esculentum*
proline transporter 2. LeProT2.

AAD25160.1 AF014808 *Lycopersicon esculentum*
proline transporter 1. LeProT1.

AAF76897.1 AF274032 *Atriplex hortensis*
proline/glycine betaine transporter.

CAB42599.1 AJ238635 *Chlorella protothecoides*
amino acid carrier. dee4.

SEQ ID NO: 526

BAA03763.1 D16247 *Nicotiana sylvestris*
RNA helicase like protein DB10.

AAD46404.1 AF096248 *Lycopersicon esculentum*
ethylene-responsive RNA helicase. ER68. putative DEAD box/RNA helicase.

AAF75791.1 AF271892 *Pisum sativum*
DEAD box protein P68. P68. RNA helicase.

AAF40306.1 AF156667 *Vigna radiata*
RNA helicase. VRH1.

CAA68193.1 X99937 *Spinacia oleracea*
RNA helicase. prh75. DEAD-box protein; homologous to X99938.

AAG13612.1 AC078840 *Oryza sativa*
putative RNA helicase. OSJNBb0073N24.12.

AAG34876.1 AF261021 *Nicotiana tabacum*
putative chloroplast RNA helicase VDL isoform 1. VDL. alternatively spliced.

AAG34873.1 AF261020 *Nicotiana tabacum*
putative chloroplast RNA helicase VDL isoform 1. VDL. essential for chloroplast
development; may be involved in post-transcriptional regulation.

AAG34879.1 AF261024 *Nicotiana tabacum*
putative chloroplast RNA helicase VDL' isoform 1. VDL'. alternatively spliced.

AAD20980.1 AF079782 *Zea mays*
ATPase and RNA helicase. translation initiation factor 4A2. tif4A2.

AAG34882.1 AF261027 *Nicotiana tabacum*
putative chloroplast RNA helicase VDL' isoform 4. VDL'. alternatively spliced.

BAA95705.1	AB042644	Oryza sativa	DEAD box RNA helicase OsPL10b. OsPL10b.
BAA95704.1	AB042643	Oryza sativa	DEAD box RNA helicase OsPL10a. OsPL10a.
AAG34883.1	AF261028	Nicotiana tabacum	putative chloroplast RNA helicase VDL' isoform 5. VDL'. alternatively spliced.
AAG38493.1	AF261032	Nicotiana tabacum	putative chloroplast RNA helicase VDL' isoform 1. VDL'. alternatively spliced.
AAG34884.1	AF261029	Nicotiana tabacum	putative chloroplast RNA helicase VDL' isoform 6. VDL'. alternatively spliced.
AAG38496.1	AF261032	Nicotiana tabacum	putative chloroplast RNA helicase VDL' isoform 4. VDL'. alternatively spliced.
AAG38497.1	AF261032	Nicotiana tabacum	putative chloroplast RNA helicase VDL' isoform 5. VDL'. alternatively spliced.
AAG38498.1	AF261032	Nicotiana tabacum	putative chloroplast RNA helicase VDL' isoform 6. VDL'. alternatively spliced.
AAG38500.1	AF261032	Nicotiana tabacum	putative chloroplast RNA helicase VDL' isoform 8. VDL'. alternatively spliced.
AAG34886.1	AF261031	Nicotiana tabacum	putative chloroplast RNA helicase VDL' isoform 8. VDL'. alternatively spliced.
AAG48833.1	AC084218	Oryza sativa	similar to Arabidopsis thaliana DNA helicase (AJ404475).
SEQ ID NO: 528			
CAA65536.1	X96761	Sporobolus stapfianus	sulphate transporter protein.
AAK27688.1	AF347614	Lycopersicon esculentum	sulfate transporter 2. ST2.
AAK27687.1	AF347613	Lycopersicon esculentum	sulfate transporter 1. ST1.
CAA57711.1	X82256	Stylosanthes hamata	high affinity sulphate transporter. SHST2.
AAG41419.1	AF309643	Solanum tuberosum	high affinity sulfate transporter type 1. ST1.
CAA57710.1	X82255	Stylosanthes hamata	high affinity sulphate transporter. SHST1.
AAK35215.1	AF355602	Zea mays	sulfate transporter ST1.
CAA65291.1	X96431	Hordeum vulgare	high affinity sulphate transporter. HVST1.
AAA97952.1	U52867	Hordeum vulgare	high affinity sulfate transporter HVST1.

CAB42985.1 AJ238244 *Aegilops tauschii*
putative plasma membrane sulfate transport. putative high affinity sulfate transporter. st1.

CAB42986.1 AJ238245 *Aegilops tauschii*
putative plasma membrane sulfate transport. putative high affinity sulfate transporter. st2.

CAA57831.1 X82454 *Stylosanthes hamata*
low affinity sulphate transporter. SHST3.

SEQ ID NO: 531

AAK00436.1 AC060755 *Oryza sativa*
putative zinc finger protein. OSJNBa0003O19.23.

BAA85438.1 AP000616 *Oryza sativa*
similar to RING-H2 finger protein RHA1a (AF078683).

AAG43550.1 AF211532 *Nicotiana tabacum*
Avr9/Cf-9 rapidly elicited protein 132. ACRE132. similar to RING finger proteins.

BAA90357.1 AP001080 *Oryza sativa*
EST AU070319(S10788) corresponds to a region of the predicted gene. Similar to RING-H2 finger protein RHA2b (AC006200).

SEQ ID NO: 532

BAA81751.1 AB017517 *Marchantia polymorpha*
calcium-dependent protein kinase. CDPK1. CDPK-B; alternative splicing.

BAA13232.1 D87042 *Zea mays*
Calcium-dependent protein kinase.

BAA81749.1 AB017515 *Marchantia polymorpha*
calcium-dependent protein kinase. CDPK1. CDPK-B; alternative splicing.

BAA81750.1 AB017516 *Marchantia polymorpha*
calcium-dependent protein kinase. CDPK1. CDPK-A; alternative splicing.

BAA85396.1 AP000615 *Oryza sativa*
ESTs C22369(C12239), C22370(C12239), AU057852(S21844), AU057853(S21844)
correspond to a region of the predicted gene.; similar to calcium dependent protein kinase.
(AF048691).

CAA57156.1 X81393 *Oryza sativa*
calcium-dependent protein kinase. OSCPKII.

AAC05270.1 AF048691 *Oryza sativa*
calcium dependent protein kinase. CDPK12.

AAB49984.1 U90262 *Cucurbita pepo*
calcium-dependent calmodulin-independent protein kinase CDPK. cpCPK1. serine/threonine
protein kinase that is activated by direct binding of calcium.

AAB70706.1 U82087 *Tortula ruralis*
calmodulin-like domain protein kinase. TrCPK1.

AAG46110.1 AC073166 *Oryza sativa*
calcium-dependent protein kinase. OSJNBb0064P21.2.

BAA02698.1 D13436 *Oryza sativa*
calcium-dependent protein kinase. spk.

BAA81748.1	AB017515	Marchantia polymorpha	calcium-dependent protein kinase. CDPK1. CDPK-A; alternative splicing.
CAA07481.1	AJ007366	Zea mays	calcium-dependent protein kinase.
AAB80692.1	U69173	Glycine max	calmodulin-like domain protein kinase isoenzyme beta. CDPK beta.
AAC49405.1	U08140	Vigna radiata	calcium dependent protein kinase. CDPK.
BAA12338.1	D84408	Zea mays	calcium dependent protein kinase. ZmCDPK1.
AAA33443.1	L15390	Zea mays	calcium-dependent protein kinase. CDPK.
CAA57157.1	X81394	Oryza sativa	calcium-dependent protein kinase. OSCPK2.
BAB21081.1	AP002819	Oryza sativa	putative calcium-dependent protein kinase. P0501G01.10.
BAA12715.1	D85039	Zea mays	calcium-dependent protein kinase.
CAA65500.1	X96723	Medicago sativa	protein kinase. CDPK.
AAC25423.1	AF072908	Nicotiana tabacum	calcium-dependent protein kinase. CDPK1.
AAA69507.1	U28376	Zea mays	calcium-dependent protein kinase. MZECDPK2.
BAA13440.1	D87707	Ipomoea batatas	calcium dependent protein kinase. CDPK.
AAD28192.2	AF115406	Solanum tuberosum	calcium-dependent protein kinase. CDPK; catalytic domain.
AAB80693.1	U69174	Glycine max	calmodulin-like domain protein kinase isoenzyme gamma. CDPK gamma.
AAA61682.1	L27484	Zea mays	calcium-dependent protein kinase. CDPK.
AAD17800.1	AF090835	Mesembryanthemum crystallinum	Ca ²⁺ -dependent protein kinase. CPK1. serine/threonine protein kinase.
CAA39936.1	X56599	Daucus carota	calcium- dependent protein kinase. DcPK431.
AAK26164.1	AY027885	Cucumis sativus	calcium-dependent calmodulin-independent protein kinase 5. CDPK5. CsCDPK5.
AAB88537.1	AF035944	Fragaria x ananassa	calcium-dependent protein kinase. MAX17.
AAF21062.1	AF216527	Dunaliella tertiolecta	calcium-dependent protein kinase. CPK1; CDPK.

CAA89202.1	Z49233	<i>Chlamydomonas eugametos</i> calcium-stimulated protein kinase.
AAC32116.1	AF051211	<i>Picea mariana</i> probable calcium dependent protein kinase. Sb15. similar to <i>Vigna radiata</i> calcium dependent protein kinase encoded by U08140.
AAF23900.1	AF194413	<i>Oryza sativa</i> calcium-dependent protein kinase. CDPK1. OsCDPK1.
AAF23901.2	AF194414	<i>Oryza sativa</i> calcium-dependent protein kinase. CDPK5. OsCDPK5.
CAB46228.1	Y18055	<i>Arachis hypogaea</i> calcium dependent protein kinase. CDPK.
AAC78558.1	AF030879	<i>Solanum tuberosum</i> protein kinase CPK1.
CAA58750.1	X83869	<i>Daucus carota</i> CDPK-related protein kinase. CRK (or PK421).
AAB47181.1	S82324	<i>Zea mays</i> /gene="calcium/calmodulin-dependent protein kinase. This sequence comes from Fig. 1.
BAA12691.1	D84507	<i>Zea mays</i> CDPK-related protein kinase. Does not require calcium for its activity (by similarity).
BAA22410.1	D38452	<i>Zea mays</i> calcium-dependent protein kinase-related kinase.
BAA12692.1	D84508	<i>Zea mays</i> CDPK-related protein kinase. Does not require calcium for its activity.
AAG01179.1	AF289237	<i>Zea mays</i> calcium/calmodulin dependent protein kinase MCK2. MCK2.
AAC24961.1	AF009337	<i>Tradescantia virginiana</i> CDPK-related protein kinase. CRK1.
BAA90814.1	AP001168	<i>Oryza sativa</i> ESTs AU030197(E50746),AU030196(E50746) correspond to a region of the predicted gene.; Similar to calcium-dependent calmodulin-independent protein kinase CDPK (U90262).
AAC49008.1	U24188	<i>Lilium longiflorum</i> calcium/calmodulin-dependent phosphorylation activity. calcium/calmodulin-dependent protein kinase. CCaMK. serine/threonine kinase; binds to calcium and calmodulin.
AAF19402.1	AF203480	<i>Lycopersicon esculentum</i> phosphoenolpyruvate carboxylase kinase. protein kinase; member of Ca ²⁺ /CaM kinase family; lacks the autoinhibitory region and EF hands.
SEQ ID NO: 535		
AAK19619.1	AF336286	<i>Gossypium hirsutum</i> GHMYB9. ghmyb9. similar to myb.
CAA64614.1	X95296	<i>Lycopersicon esculentum</i> transcription factor. THM27. myb-related.
CAA50224.1	X70879	<i>Hordeum vulgare</i> MybHv1. myb1.

CAA50222.1	X70877	Hordeum vulgare	MybHv1. myb1.
AAA33067.1	L04497	Gossypium hirsutum	MYB A; putative.
CAA50221.1	X70876	Hordeum vulgare	MybHv5. myb2.
BAA23337.1	D88617	Oryza sativa	transfactor. OSMYB1. Osmyb1.
BAA23338.1	D88618	Oryza sativa	transfactor. OSMYB2. Osmyb2.
AAC04720.1	AF034134	Gossypium hirsutum	putative MYB-like transcription factor. MYB-like DNA-binding domain protein. CmY-O. similar to MYB A encoded by GenBank Accession Number L04497.
CAA72218.1	Y11415	Oryza sativa	myb.
CAA50225.1	X70880	Hordeum vulgare	MybHv5. myb2.
AAA82943.1	U39448	Picea mariana	MYB-like transcriptional factor MBF1. putative DNA binding region highly similar to the maize C1.
CAA78386.1	Z13996	Petunia x hybrida	DNA binding protein; transcriptional activator. protein 1. myb.Ph3. Product related to animal myb proto-oncoproteins. Sequence from nucleotide 992 is not included in clone cPF1 and has been obtained by PCR amplification of cDNA.
BAA81732.1	AB029161	Glycine max	GmMYB29A2.
AAK19616.1	AF336283	Gossypium hirsutum	GHMYB25. ghmyb25. similar to myb; contains an unspliced intron.
AAK19611.1	AF336278	Gossypium hirsutum	BNLGH1233. bnlghi6233. similar to myb.
AAK19617.1	AF336284	Gossypium hirsutum	GHMYB36. ghmyb36. similar to myb.
BAA93038.1	AP001552	Oryza sativa	EST AU082058(C12976) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana putative transcription factor (AF062916).
AAK19615.1	AF336282	Gossypium hirsutum	GHMYB10. ghmyb10. similar to myb.
BAB39987.1	AP003020	Oryza sativa	putative transcription factor (myb). P0498A12.16. contains ESTs AU097474(S5037),D40175(S1959).
BAB39972.1	AP003018	Oryza sativa	putative transcription factor (myb). OSJNBa0004B13.27. contains ESTs AU097474(S5087),D40175(S1959).

CAB43399.1	AJ006292	<i>Antirrhinum majus</i>	Myb-related transcription factor mixta-like 1. mybml1.
CAA72185.1	Y11350	<i>Oryza sativa</i>	myb factor. myb.
AAF22256.1	AF161711	<i>Pimpinella brachycarpa</i>	myb-related transcription factor.
AAG13574.1	AC037425	<i>Oryza sativa</i>	myb factor. OSJNBa0055P24.4.
BAA81731.1	AB029160	<i>Glycine max</i>	GmMYB29A1.
BAA81730.1	AB029159	<i>Glycine max</i>	GmMYB29A1.
CAA72186.1	Y11351	<i>Oryza sativa</i>	myb factor. myb.
CAA67600.1	X99210	<i>Lycopersicon esculentum</i>	myb-related transcription factor. THM16.
CAA75509.1	Y15219	<i>Oryza sativa</i> subsp. <i>indica</i>	transcriptional activator. C1.
AAC04718.1	AF034132	<i>Gossypium hirsutum</i>	putative MYB-like transcription factor. MYB-like DNA-binding domain protein. Cmy-J. similar to MYB A encoded by GenBank Accession Number L04497.
CAA78387.1	Z13997	<i>Petunia x hybrida</i>	DNA-binding protein, transcriptional activator. protein 2. myb.Ph2. related to animal myb proto-oncoproteins.
BAA81736.1	AB029165	<i>Glycine max</i>	GmMYB29B2.
AAK19618.1	AF336285	<i>Gossypium hirsutum</i>	GHMYB38. ghmyb38. similar to myb.
CAA72217.1	Y11414	<i>Oryza sativa</i>	myb.
AAC49394.1	U57002	<i>Zea mays</i>	P protein. P. allele P-wr; Myb-like transcriptional regulator with a putative zinc-finger at the C-terminal.
AAA33500.1	M73028	<i>Zea mays</i>	myb-like transcription factor. P.
BAB20661.1	AP002871	<i>Oryza sativa</i>	putative myb-related protein P. P0475H04.31.
AAG36774.1	AF210616	<i>Zea mays</i>	P2 protein. P2. myb-like transcriptional factor; similar to <i>Zea mays</i> P gene.
BAA88222.1	AB028650	<i>Nicotiana tabacum</i>	myb-related transcription factor LBM2. lbm2.
BAA81733.2	AB029162	<i>Glycine max</i>	GmMYB29A2.

BAA23339.1 D88619 *Oryza sativa*
transfactor. OSMYB3. Osmyb3.

BAA88224.1 AB028652 *Nicotiana tabacum*
myb-related transcription factor LBM4. lbm4.

BAA88221.1 AB028649 *Nicotiana tabacum*
myb-related transcription factor LBM1. lbm1.

AAB41101.1 U72762 *Nicotiana tabacum*
transcription factor Myb1. myb1. TMV-inducible Myb homolog; contains helix-turn-helix motif; contains redox-sensitive cysteine.

SEQ ID NO: 536

CAA70968.1 Y09825 *Solanum tuberosum*
amino acid transporter. AAP1. transmembrane protein.

AAF15946.1 AF061436 *Vicia faba*
amino acid transporter c. AAPC.

CAA70969.1 Y09826 *Solanum tuberosum*
amino acid transporter. AAP2. transmembrane protein.

AAB96830.1 U64823 *Nicotiana sylvestris*
amino acid transporter. amino acid permease. nsaap1.

CAA07563.1 AJ007574 *Ricinus communis*
amino acid carrier. aap1.

AAB48944.1 U31932 *Nicotiana sylvestris*
amino acid permease 1. NSAAP1. amino acid transporter; Method: conceptual translation supplied by author.

AAD16015.1 AF080544 *Nepenthes alata*
amino acid transporter. AAP3.

CAA70778.1 Y09591 *Vicia faba*
amino acid transporter.

AAF15944.1 AF061434 *Vicia faba*
amino acid transporter a. AAPA.

AAF15945.1 AF061435 *Vicia faba*
amino acid transporter b. AAPB.

AAF76897.1 AF274032 *Atriplex hortensis*
proline/glycine betaine transporter.

AAD16014.1 AF080543 *Nepenthes alata*
amino acid transporter. AAP2.

AAD25161.1 AF014809 *Lycopersicon esculentum*
proline transporter 2. LeProT2.

CAA10608.1 AJ132228 *Ricinus communis*
amino acid carrier. aap3.

SEQ ID NO: 537

BAA89009.1 AB027455 *Petunia x hybrida*
anthocyanin 5-O-glucosyltransferase. PH1.

BAA36423.1	AB013598	Verbena x hybrida	UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.
BAA36421.1	AB013596	Perilla frutescens	UDP-glucose:anthocynin 5-O-glucosyltransferase. PF3R4.
BAB07962.1	AP002524	Oryza sativa	putative anthocyanin 5-O-glucosyltransferase. P0406H10.16. contains ESTs AU067881(C10481),AU067882(C10481).
BAA36422.1	AB013597	Perilla frutescens	UDP-glucose:anthocyanin 5-O-glucosyltransferase homologue. PF3R6.
BAA93039.1	AB033758	Citrus unshiu	limonoid UDP-glucosyltransferase. LGTase.
AAF61647.1	AF190634	Nicotiana tabacum	UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.
AAF98390.1	AF287143	Brassica napus	catalyzes the transfer of glucose from UDP-glucose to sinapate and some other hydroxycinnamates (4-coumarate, caffeate, ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.
AAK16175.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.15.
AAF17077.1	AF199453	Sorghum bicolor	UDP-glucose glucosyltransferase. UDP-glucose:p-hydroxymandelonitrile-o-glucosyltransferase.
AAK16172.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.14.
BAA83484.1	AB031274	Scutellaria baicalensis	UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.
AAK16181.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.16.
AAG25643.1	AF303396	Phaseolus vulgaris	UDP-glucosyltransferase HRA25. putative; defense associated.
AAK16178.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.5.
AAD21086.1	AF127218	Forsythia x intermedia	adds glucose residue to position 3 of flavonoid compounds. flavonoid 3-O-glucosyltransferase. UFGT.
BAA12737.1	D85186	Gentiana triflora	UDP-glucose:flavonoid-3-glucosyltransferase.
AAK28303.1	AF346431	Nicotiana tabacum	phenylpropanoid:glucosyltransferase 1. togt1. glucosyltransferase.
CAB56231.1	Y18871	Dorotheanthus bellidiformis	betanidin-5-O-glucosyltransferase.
CAA54612.1	X77462	Manihot esculenta	UTP-glucose glucosyltransferase. CGT5.

BAB41019.1	AB047092	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT1.
BAB41020.1	AB047093	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT2.
AAB36653.1	U32644	Nicotiana tabacum	immediate-early salicylate-induced glucosyltransferase. IS5a.
BAB41025.1	AB047098	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT1.
BAB41023.1	AB047096	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT1.
BAB41022.1	AB047095	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT2.
BAB41021.1	AB047094	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT1.
BAA19659.1	AB002818	Perilla frutescens	flavonoid 3-O-glucosyltransferase. UDP glucose.
BAB41026.1	AB047099	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT2.
BAB41024.1	AB047097	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT2.
AAK16180.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.21.
AAK28304.1	AF346432	Nicotiana tabacum	phenylpropanoid:glucosyltransferase 2. togt2. glucosyltransferase.
AAB36652.1	U32643	Nicotiana tabacum	immediate-early salicylate-induced glucosyltransferase. IS10a.
BAB41017.1	AB047090	Vitis labrusca x Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT1. The gene was derived from one of the parents V. labruscana cv. Ishiharawase.
BAA89008.1	AB027454	Petunia x hybrida	anthocyanidin 3-O-glucosyltransferase. PGT8.
CAA59450.1	X85138	Lycopersicon esculentum	twil. homologous to glucosyltransferases.
CAA54614.1	X77464	Manihot esculenta	UTP-glucose glucosyltransferase. CGT7.
CAA54611.1	X77461	Manihot esculenta	UTP-glucose glucosyltransferase. CGT2.
CAA54613.1	X77463	Manihot esculenta	UTP-glucose glucosyltransferase. CGT6.
SEQ ID NO: 540			
AAK27688.1	AF347614	Lycopersicon esculentum	sulfate transporter 2. ST2.

AAG41419.1 AF309643 *Solanum tuberosum*
high affinity sulfate transporter type 1. ST1.

AAK27687.1 AF347613 *Lycopersicon esculentum*
sulfate transporter 1. ST1.

AAA97952.1 U52867 *Hordeum vulgare*
high affinity sulfate transporter HVST1.

CAA57711.1 X82256 *Stylosanthes hamata*
high affinity sulphate transporter. SHST2.

CAA65291.1 X96431 *Hordeum vulgare*
high affinity sulphate transporter. HVST1.

CAA57710.1 X82255 *Stylosanthes hamata*
high affinity sulphate transporter. SHST1.

CAB42985.1 AJ238244 *Aegilops tauschii*
putative plasma membrane sulfate transport. putative high affinity sulfate transporter. st1.

AAK35215.1 AF355602 *Zea mays*
sulfate transporter ST1.

CAB42986.1 AJ238245 *Aegilops tauschii*
putative plasma membrane sulfate transport. putative high affinity sulfate transporter. st2.

CAA65536.1 X96761 *Sporobolus stapfianus*
sulphate transporter protein.

CAA57831.1 X82454 *Stylosanthes hamata*
low affinity sulphate transporter. SHST3.

CAA11413.1 AJ223495 *Brassica juncea*
sulfate permease. sp1.

AAB94543.1 AF016306 *Zea mays*
sulfate permease.

SEQ ID NO: 541

AAF36491.1 AF129479 *Hordeum vulgare*
HAK2. HAK2. similar to *Hordeum vulgare* K⁺ transporter HAK1.

BAB32443.1 AB055630 *Phragmites australis*
high-affinity potassium transporter. PcnHAK1.

BAB32444.1 AB055631 *Phragmites australis*
high-affinity potassium transporter. PceHAK1A.

BAB32445.1 AB055632 *Phragmites australis*
high-affinity potassium transporter. PceHAK1B.

BAB32442.1 AB055629 *Phragmites australis*
high-affinity potassium transporter. PcuHAK1.

AAC39315.1 AF025292 *Hordeum vulgare*
putative high-affinity potassium transporter. HvHAK1.

AAF36497.1 AF129485 *Oryza sativa*
HAK4. HAK4. OsHAK4; similar to *Hordeum vulgare* K⁺ transporter HAK1.

AAF36496.1 AF129484 *Hordeum vulgare*
HAK4. HAK4. HvHAK4; similar to *Hordeum vulgare* K⁺ transporter HAK1.

CAC14883.1 AJ297888 *Hordeum vulgare*
putative potassium transporter. hak1.

CAC14787.1 AJ297886 *Hordeum vulgare*
putative potassium transporter. hak1.

AAF36492.1 AF129480 *Hordeum vulgare*
HAK1B. HAK1B. HvHAK1B; similar to *Hordeum vulgare* K⁺ transporter HAK1.

CAC15061.1 AJ300161 *Hordeum vulgare*
potassium transporter. hak4.

SEQ ID NO: 542

AAA91063.1 M88254 *Hevea brasiliensis*
ethylene-inducible protein. ER1.

SEQ ID NO: 546

CAA75386.1 Y15113 *Morinda citrifolia*
3-deoxy-D-arabino-heptulosonate 7-phosphate synthase. DS3. 2-dehydro-3-deoxyphosphoheptonate aldolase.

CAA79855.1 Z21792 *Lycopersicon esculentum*
phospho-2-dehydro-3-deoxyheptonate aldolase.

CAA79856.1 Z21793 *Lycopersicon esculentum*
phospho-2-dehydro-3-deoxyheptonate aldolase.

SEQ ID NO: 548

BAA96751.1 AP002521 *Oryza sativa*
Similar to *Arabidopsis thaliana* chromosome4, BAC clone T16H5; lectin like protein (AL024486).

SEQ ID NO: 551

BAB19096.1 AP002839 *Oryza sativa*
putative DNA-binding protein homolog. P0688A04.2.

BAB19075.1 AP002744 *Oryza sativa*
putative DNA-binding protein homolog. P0006C01.17.

AAK16170.1 AC079887 *Oryza sativa*
putative DNA binding protein. OSJNBa0040E01.4.

AAD32677.1 AF140554 *Avena sativa*
DNA-binding protein WRKY1. wrky1. putative transcription factor.

AAD16139.1 AF096299 *Nicotiana tabacum*
DNA-binding protein 2. WRKY2. transcription factor.

CAB97004.1 AJ278507 *Solanum tuberosum*
putative transcription factor. WRKY DNA binding protein. WRKY1.

CAA88326.1 Z48429 *Avena fatua*
binds conserved cis-element from cereal alpha-Amy2 promoters. DNA-binding protein.

AAC49527.1 U48831 *Petroselinum crispum*
WRKY1. contains two WRKY domains; WRKY-type DNA-binding protein; sequence-specific DNA-binding protein.

AAC49529.1	U58540	Petroselinum crispum	WRKY2. Contains two WRKY domains; WRKY-type DNA-binding protein.
AAK16171.1	AC079887	Oryza sativa	putative DNA-binding protein. OSJNBa0040E01.10.
AAC37515.1	L44134	Cucumis sativus	SPF1-like DNA-binding protein.
AAD16138.1	AF096298	Nicotiana tabacum	DNA-binding protein 1. WRKY1. transcription factor.
AAD38283.1	AC007789	Oryza sativa	putative WRKY DNA binding protein. OSJNBa0049B20.9.
BAB18313.1	AP002865	Oryza sativa	putative WRKY DNA binding protein. P0034C11.1. contains EST C26525(C12525).
BAB40073.1	AP003074	Oryza sativa	putative WRKY DNA binding protein. OSJNBa0004G10.20. contains EST C26525(C12525).
AAC49528.1	U56834	Petroselinum crispum	DNA-binding. WRKY3. WRKY-type DNA-binding protein.
BAA77358.1	AB020023	Nicotiana tabacum	WRKY domain Zn-finger type DNA-binding protein. DNA-binding protein NtWRKY3.
AAG46150.1	AC018727	Oryza sativa	putative DNA-binding protein. OSJNBa0056G17.18.
CAA88331.1	Z48431	Avena fatua	binds conserved cis-element from cereal alpha-Amy2 promoters. DNA-binding protein.
AAD32676.1	AF140553	Avena sativa	DNA-binding protein WRKY3. wrky3. putative transcription factor.
CAB66338.1	AJ279697	Betula pendula	wrky-type DNA binding protein. wrky.
AAF61863.1	AF193770	Nicotiana tabacum	DNA-binding protein 3. WRKY3. transcription factor.
AAF61864.1	AF193771	Nicotiana tabacum	DNA-binding protein 4. WRKY4. transcription factor.
AAD27591.1	AF121354	Petroselinum crispum	binds sequence specifically to W Boxes (TTGACC). transcription factor. WRKY3. sequence specific DNA-binding protein.
BAA87069.1	AB035271	Matricaria chamomilla	elicitor-induced DNA-binding protein homolog. McWRKY1.
SEQ ID NO: 553			
AAF34428.1	AF172282	Oryza sativa	receptor-like protein kinase. DUPR11.18.
BAA94518.1	AP001800	Oryza sativa	Similar to Arabidopsis thaliana chromosome 2 section 111 of 255; putative receptor-like protein kinase (AC002392).
BAB07904.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.12.

BAA94516.1	AP001800	Oryza sativa	Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAB07906.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.14.
BAA94517.1	AP001800	Oryza sativa	Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAB07905.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.13.
BAA94528.1	AP001800	Oryza sativa	Similar to Arabidopsis thaliana chromosome 2 BAC T20K24; putative receptor-like protein kinase (AC002392).
BAA94529.2	AP001800	Oryza sativa	Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
CAA67145.1	X98520	Brassica oleracea	receptor-like kinase. SFR2.
CAA73133.1	Y12530	Brassica oleracea	serine /threonine kinase. ARLK.
CAB89179.1	AJ245479	Brassica napus subsp. napus	ser /thr kinase. S-locus receptor kinase. srk.
AAA33008.1	M97667	Brassica napus	serine/threonine kinase receptor.
AAC23542.1	U20948	Ipomoea trifida	receptor protein kinase. IRK1.
BAA23676.1	AB000970	Brassica rapa	receptor kinase 1. BcRK1.
BAA92836.1	AB032473	Brassica oleracea	S18 S-locus receptor kinase. SRK18.
CAB41878.1	Y18259	Brassica oleracea	SRK5 protein. SRK5. receptor-like kinase.
CAB41879.1	Y18260	Brassica oleracea	SRK15 protein. SRK15. receptor-like kinase.
BAA21132.1	D88193	Brassica rapa	S-receptor kinase. SRK9 (B.c).
BAA06285.1	D30049	Brassica rapa	S-receptor kinase SRK9.
CAA74662.1	Y14286	Brassica oleracea	SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
CAA79355.1	Z18921	Brassica oleracea	S-receptor kinase-like protein.
BAB21001.1	AB054061	Brassica rapa	S locus receptor kinase. SRK22.

AAA33915.1 L27821 *Oryza sativa*
receptor type serine/threonine kinase. protein kinase.
BAA92954.1 AP001551 *Oryza sativa*
Similar to *Oryza sativa* protein kinase (OSPK10) mRNA. (L27821).

SEQ ID NO: 554

CAC05658.1 AJ250919 *Brassica napus*
endopolygalacturonase. pegaz.
CAC05657.1 AJ250918 *Brassica napus*
endopolygalacturonase. pgaz.
CAA65072.1 X95800 *Brassica napus*
polygalacturonase.
CAA90272.1 Z49971 *Brassica napus*
Hydrolytic enzyme. Polygalacturonase. pga.
CAA54448.1 X77231 *Prunus persica*
polygalacturonase. PG.
AAC14453.1 L12019 *Actinidia deliciosa*
polygalacturonase.
AAF71160.1 AF152758 *Actinidia chinensis*
polygalacturonase A. PGA.
AAA34178.1 M37304 *Lycopersicon esculentum*
polygalacturonase.
CAA32235.1 X14074 *Lycopersicon esculentum*
polygalacturonase.
CAA29148.1 X05656 *Lycopersicon esculentum*
polygalacturonase (AA 1-457).
AAA32914.1 L06094 *Persea americana*
cell wall degradation. polygalacturonase.
CAA47055.1 X66426 *Persea americana*
polygalacturonase.
AAC26512.1 AF062467 *Cucumis melo*
polygalacturonase precursor. MPG3.
CAA11846.1 AJ224147 *Rubus idaeus*
polygalacturonase. RAS3.
AAF61444.1 AF138858 *Lycopersicon esculentum*
hydrolyses polygalacturonic acid. polygalacturonase. XOPG1.
BAA88472.1 AB035890 *Cucumis sativus*
polygalacturonase. CUPG1.
AAD46483.1 AF128266 *Glycine max*
polygalacturonase PG1.
AAD46484.1 AF128267 *Glycine max*
polygalacturonase PG2.

AAC28905.1	AF001002	Lycopersicon esculentum	hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 4. TAPG4. expressed in abscission.
AAC28906.1	AF001003	Lycopersicon esculentum	hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 5. TAPG5. expressed in abscission.
AAC28903.1	AF001000	Lycopersicon esculentum	hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 1. TAPG1. expressed in abscission.
AAA80489.1	U23053	Lycopersicon esculentum	polygalacturonase precursor.
AAC64184.1	AF095577	Prunus persica	endopolygalacturonase.
AAC28902.2	AF000999	Lycopersicon esculentum	hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 3. TAPG3. expressed in abscission.
AAB09575.1	U70480	Lycopersicon esculentum	abscission polygalacturonase. TAPG2.
AAC28904.1	AF001001	Lycopersicon esculentum	hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 2. TAPG2. expressed in abscission.
CAA54150.1	X76735	Prunus persica	endopolygalacturonase.
AAC70951.1	AF072732	Lycopersicon esculentum	hydrolyzes pectin in the cell wall and middle lamella. polygalacturonase 7. specifically and abundantly expressed in pistils.
AAC26511.1	AF062466	Cucumis melo	polygalacturonase precursor. MPG2.
AAB09576.1	U70481	Lycopersicon esculentum	abscission polygalacturonase. TAPG4.
AAC28947.1	AF029230	Lycopersicon esculentum	polygalacturonase. TPG6.
AAA82167.1	U09717	Gossypium hirsutum	polygalacturonase.
AAA58322.1	U09805	Gossypium barbadense	polygalacturonase.
CAA47052.1	X66422	Zea mays	polygalacturonase. PG.
AAG14416.1	AF248538	Nicotiana tabacum	NTS1 protein. similar to polygalacturonase.
CAB42886.1	AJ238848	Phleum pratense	polygalacturonase. pg.

CAA40850.1	X57627	Zea mays	polygalacturonase.
CAA46679.1	X65844	Zea mays	polygalacturonase. PGg6.
CAA40910.1	X57743	Zea mays	polygalacturonase.
CAA44249.1	X62385	Zea mays	polygalacturonase.
CAA45751.1	X64408	Zea mays	polygalacturonase. PG. pollen-preferentially expressed.
CAA40851.1	X57628	Zea mays	polygalacturonase.
CAA46680.1	X65845	Zea mays	polygalacturonase. PGg14.
AAC26510.1	AF062465	Cucumis melo	polygalacturonase precursor. MPG1.
SEQ ID NO: 556			
CAA51734.1	X73301	Vigna mungo	alpha-amylase. amyVml.
CAA37217.1	X53049	Vigna mungo	alpha-amylase (AA 1-421).
BAA33879.1	AB015131	Phaseolus vulgaris	alpha-amylase.
AAA16513.1	U06754	Cuscuta reflexa	starch hydrolysis. alpha amylase precursor. CUS AMY2.
AAA98615.1	J04202	Hordeum vulgare	alpha-amylase. Amy46. precursor.
AAA98790.1	K02637	Hordeum vulgare	alpha-amylase type B. Amy6-4. precursor.
CAA33298.1	X15226	Hordeum vulgare	alpha-amylase.
AAA33885.1	M24286	Oryza sativa	alpha-amylase (EC 3.2.1.1).
CAA34516.1	X16509	Oryza sativa	alpha-amylase.
CAA72144.1	Y11277	Hordeum vulgare	alpha-amylase. amy.
CAA33299.1	X15227	Hordeum vulgare	alpha amylase.
AAA32925.1	M17126	Hordeum vulgare	alpha-amylase 1.

AAA32927.1	M17128	Hordeum vulgare	alpha-amylase 2.
AAA32929.1	J01236	Hordeum vulgare	alpha-amylase type A, EC 3.2.1.1.
CAA39777.1	X56337	Oryza sativa	alpha-amylase. RAm3B.
CAA09323.1	AJ010728	Avena fatua	alpha amylase. alpha-Amy2A.
AAA33897.1	M24941	Oryza sativa	alpha-amylase precursor (EC 3.2.1.1).
CAA09324.1	AJ010729	Avena fatua	alpha-amylase. alpha-Amy2D.
CAA28803.1	X05166	Hordeum vulgare	alpha-amylase type A. Amy32b.
AAA32926.1	M17125	Hordeum vulgare	alpha-amylase 1.
CAA39778.1	X56338	Oryza sativa	alpha-amylase. RAm3C.
AAA32935.1	M15208	Hordeum vulgare	alpha-amylase.
AAA33895.1	M59351	Oryza sativa	alpha-amylase. RAm3D.
AAA33896.1	M59352	Oryza sativa	alpha-amylase. RAm3E.
AAA50161.1	L25805	Zea mays	alpha-amylase.
AAA33894.1	M74177	Oryza sativa	alpha-amylase. amy2A.
CAA72143.1	Y11276	Hordeum vulgare	alpha-amylase. amy.
CAA39776.1	X56336	Oryza sativa	alpha-amylase. RAm3A.
CAA45903.1	X64619	Oryza sativa	alpha-amylase. Amyc2. starts hydrolysis during seed germination.
AAA33886.1	M24287	Oryza sativa	alpha-amylase (EC 3.2.1.1).
AAA32928.1	M17127	Hordeum vulgare	alpha-amylase 2.
AAA32933.1	K02638	Hordeum vulgare	pre-alpha-amylase type B, EC 3.2.1.1.
AAA91883.1	M81682	Solanum tuberosum	alpha-amylase. Amy23.

AAA34259.1	M16991	Triticum aestivum
alpha-amylase.		
CAA29252.1	X05809	Triticum aestivum
alpha-amylase.		
AAA91884.1	M79328	Solanum tuberosum
alpha-amylase.		
AAF63239.1	AF153828	Malus x domestica
degrades starch. alpha-amylase. alpha-amylase by similarity.		
AAA32930.1	M10056	Hordeum vulgare
alpha-amylase type B, EC 3.2.1.1.		
AAA32931.1	K02635	Hordeum vulgare
alpha-amylase type B, EC 3.2.1.1.		
CAA36485.1	X52240	Oryza sativa
alpha-amylase. OSamy-c.		
AAA32932.1	K02636	Hordeum vulgare
alpha-amylase type B, EC 3.2.1.1.		

SEQ ID NO: 557

CAA90272.1	Z49971	Brassica napus
Hydrolytic enzyme. Polygalacturonase. pga.		
CAA65072.1	X95800	Brassica napus
polygalacturonase.		
CAA67020.1	X98373	Brassica napus
endo-polygalacturonidase.		
CAC05658.1	AJ250919	Brassica napus
endopolygalacturonase. pegaz.		
CAC05657.1	AJ250918	Brassica napus
endopolygalacturonase. pgaz.		
AAC14453.1	L12019	Actinidia deliciosa
polygalacturonase.		
AAF71160.1	AF152758	Actinidia chinensis
polygalacturonase A. PGA.		
CAA54448.1	X77231	Prunus persica
polygalacturonase. PG.		
AAA34178.1	M37304	Lycopersicon esculentum
polygalacturonase.		
CAA29148.1	X05656	Lycopersicon esculentum
polygalacturonase (AA 1-457).		
CAA32235.1	X14074	Lycopersicon esculentum
polygalacturonase.		
AAA32914.1	L06094	Persea americana
cell wall degradation. polygalacturonase.		

CAA47055.1	X66426	Persea americana	polygalacturonase.
AAC26512.1	AF062467	Cucumis melo	polygalacturonase precursor. MPG3.
CAA11846.1	AJ224147	Rubus idaeus	polygalacturonase. RAS3.
BAA88472.1	AB035890	Cucumis sativus	polygalacturonase. CUPG1.
AAF61444.1	AF138858	Lycopersicon esculentum	hydrolyses polygalacturonic acid. polygalacturonase. XOPG1.
AAA80489.1	U23053	Lycopersicon esculentum	polygalacturonase precursor.
AAC28903.1	AF001000	Lycopersicon esculentum	hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 1. TAPG1. expressed in abscission.
AAB09575.1	U70480	Lycopersicon esculentum	abscission polygalacturonase. TAPG2.
AAC28904.1	AF001001	Lycopersicon esculentum	hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 2. TAPG2. expressed in abscission.
AAC28905.1	AF001002	Lycopersicon esculentum	hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 4. TAPG4. expressed in abscission.
AAC64184.1	AF095577	Prunus persica	endopolygalacturonase.
AAD46483.1	AF128266	Glycine max	polygalacturonase PG1.
AAC28906.1	AF001003	Lycopersicon esculentum	hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 5. TAPG5. expressed in abscission.
AAD46484.1	AF128267	Glycine max	polygalacturonase PG2.
CAA54150.1	X76735	Prunus persica	endopolygalacturonase.
AAC26511.1	AF062466	Cucumis melo	polygalacturonase precursor. MPG2.
AAC28902.2	AF000999	Lycopersicon esculentum	hydrolyzes pectin in the cell wall and middle lamella of plant cells. polygalacturonase 3. TAPG3. expressed in abscission.
AAC70951.1	AF072732	Lycopersicon esculentum	hydrolyzes pectin in the cell wall and middle lamella. polygalacturonase 7. specifically and abundantly expressed in pistils.

CAA47052.1	X66422	Zea mays	polygalacturonase. PG.
AAC28947.1	AF029230	Lycopersicon esculentum	polygalacturonase. TPG6.
AAA82167.1	U09717	Gossypium hirsutum	polygalacturonase.
AAB09576.1	U70481	Lycopersicon esculentum	abscission polygalacturonase. TAPG4.
CAA40910.1	X57743	Zea mays	polygalacturonase.
CAA44249.1	X62385	Zea mays	polygalacturonase.
CAA40850.1	X57627	Zea mays	polygalacturonase.
AAG14416.1	AF248538	Nicotiana tabacum	NTS1 protein. similar to polygalacturonase.
CAA46679.1	X65844	Zea mays	polygalacturonase. PGg6.
AAC26510.1	AF062465	Cucumis melo	polygalacturonase precursor. MPG1.
AAA58322.1	U09805	Gossypium barbadense	polygalacturonase.
CAA46680.1	X65845	Zea mays	polygalacturonase. PGg14.
CAA40851.1	X57628	Zea mays	polygalacturonase.
CAA45751.1	X64408	Zea mays	polygalacturonase. PG. pollen-preferentially expressed.
CAB42886.1	AJ238848	Phleum pratense	polygalacturonase. pg.

SEQ ID NO: 559

CAB43937.1	AJ006348	Fragaria x ananassa	cell wall hydrolysis. endo-beta-1,4-glucanase. eg1.
AAC95009.1	AF074923	Fragaria x ananassa	endo-1,4-beta-glucanase precursor. Cell. 1,4-beta-glucanohydrolase.
AAC12684.1	U76725	Pinus radiata	endo-beta-1,4-glucanase. PrCell. cellulase; PRCEL1.
AAA69909.1	U13055	Lycopersicon esculentum	cell wall hydrolase. endo-1,4-beta-glucanase precursor. Cel2. cellulase.
CAA65600.1	X96856	Prunus persica	endo-beta-1,4-glucanase. ppEG1.

CAA65597.1	X96853	Prunus persica	endo-beta-1,4-glucanase. pcell.
CAA65827.1	X97189	Capsicum annuum	endo-beta-1,4-glucanase. ccel3. cellulase.
AAC62241.1	AF077339	Lycopersicon esculentum	endo-1,4-beta-glucanase. cel5. cellulase; also expressed in fruit and pistils.
BAA85150.1	AB032830	Pisum sativum	endo-1,4-beta-glucanase. EGL2.
AAA80495.1	U20590	Lycopersicon esculentum	endo-1,4-beta-glucanase precursor. cellulase.
BAB32662.1	AB055886	Atriplex lentiformis	beta-1,4-glucanase. Al-cell. cellulase.
CAA65828.1	X97190	Capsicum annuum	endo-beta-1,4-glucanase. ccel2.
AAC12685.1	U76756	Pinus radiata	endo-beta-1,4-glucanase. PrCel2. cellulase; PRCEL2.
BAA77239.1	AB025796	Populus alba	endo-1,4-beta glucanase. POPCEL2. cellulase.
CAB59900.1	AJ010950	Capsicum annuum	cell wall degradation. endo-beta-1,4-glucanase. eg2.
BAB39483.1	AB049200	Populus alba	endo-1,4-beta-glucanase. PopCel2.
BAB39482.1	AB049199	Populus alba	endo-1,4-beta glucanase. PopCell.
CAA72133.1	Y11268	Lycopersicon esculentum	endo-1,4-beta-D-glucanase. cel7.
AAA96135.1	L41046	Pisum sativum	endo-1,4-beta-glucanase. EGL1.
AAC78504.1	U34754	Phaseolus vulgaris	endo-1,4-beta-D-glucanase. cellulase.
AAA02563.1	M57400	Phaseolus vulgaris	cellulase precursor. endo-1,4-beta-D-glucanase.
CAA60737.1	X87323	Capsicum annuum	catalyzes hydrolysis of cell wall polysaccharides. cellulase. cel1. Beta-1,4-endoglycanohydrolase.
CAA65826.1	X97188	Capsicum annuum	endo-beta-1,4-glucanase. ccell. cellulase.
AAA69908.1	U13054	Lycopersicon esculentum	cell wall hydrolase. endo-1,4-beta-glucanase precursor. Cell. cellulase.
CAB43938.1	AJ006349	Fragaria x ananassa	cell wall hydrolysis. endo-beta-1,4-glucanase. eg3.

BAA96209.1 AP002094 *Oryza sativa*
EST C72268(E1328) corresponds to a region of the predicted gene. Similar to *Fragaria x ananassa* endo-beta-1,4-glucanase (AJ006349).

BAA96207.1 AP002094 *Oryza sativa*
EST C72268(E1328) corresponds to a region of the predicted gene. Similar to *Fragaria x ananassa* endo-beta-1,4-glucanase (AJ006349).

AAD08699.1 AF098292 *Lycopersicon esculentum*
endo-beta-1,4-D-glucanase. Cel8.

BAA94257.1 AB040769 *Hordeum vulgare*
endo-1,4-beta-glucanase Cel1. Cell.

AAC49704.1 U78526 *Lycopersicon esculentum*
endo-1,4-beta-glucanase. Cel3.

CAB51903.1 AJ242807 *Brassica napus*
endo-1,4-beta-D-glucanase. Cell6. cellulase.

AAA20082.1 U00730 *Glycine max*
CMCase; cellulase; endo-1,4-beta-D-glucanase.

CAA11301.1 AJ223386 *Fragaria x ananassa*
endo-beta-1,4-glucanase. faEG1. partial cDNA obtained by RT-PCR amplification.

CAA11302.1 AJ223387 *Fragaria x ananassa*
endo-beta-1,4-glucanase. partial cDNA obtained by RT-PCR amplification.

BAA21111.1 D88417 *Gossypium hirsutum*
endo-1,4-beta-glucanase.

AAA20083.1 U00731 *Glycine max*
CMCase; cellulase; endo-1,4-beta-D-glucanase.

SEQ ID NO: 560

AAB97617.1 U83687 *Apium graveolens*
NADPH-dependent mannose 6-phosphate reductase. m6pr. aldo-keto reductase; similar to aldose 6-phosphate reductase also known as NADP-sorbitol-6-phosphate dehydrogenase encoded by GenBank Accession Number D11080.

AAC97607.1 AF057134 *Malus x domestica*
synthesizes sorbitol, a major photosynthetic product in many members of the Rosaceae family. NADP-dependent sorbitol 6-phosphate dehydrogenase. S6PDH.

BAA01853.1 D11080 *Malus x domestica*
NADP-dependent D-sorbitol-6-phosphate dehydrogenase. S6PDH.

SEQ ID NO: 561

CAB43938.1 AJ006349 *Fragaria x ananassa*
cell wall hydrolysis. endo-beta-1,4-glucanase. eg3.

BAA96209.1 AP002094 *Oryza sativa*
EST C72268(E1328) corresponds to a region of the predicted gene. Similar to *Fragaria x ananassa* endo-beta-1,4-glucanase (AJ006349).

BAA96207.1 AP002094 *Oryza sativa*
EST C72268(E1328) corresponds to a region of the predicted gene. Similar to *Fragaria x ananassa* endo-beta-1,4-glucanase (AJ006349).

AAD08699.1	AF098292	Lycopersicon esculentum	endo-beta-1,4-D-glucanase. Cel8.
BAA21111.1	D88417	Gossypium hirsutum	endo-1,4-beta-glucanase.
CAA65828.1	X97190	Capsicum annuum	endo-beta-1,4-glucanase. ccel2.
CAB59900.1	AJ010950	Capsicum annuum	cell wall degradation. endo-beta-1,4-glucanase. eg2.
AAC95009.1	AF074923	Fragaria x ananassa	endo-1,4-beta-glucanase precursor. Cell. 1,4-beta-glucanohydrolase.
CAB43937.1	AJ006348	Fragaria x ananassa	cell wall hydrolysis. endo-beta-1,4-glucanase. eg1.
AAA80495.1	U20590	Lycopersicon esculentum	endo-1,4-beta-glucanase precursor. cellulase.
BAA85150.1	AB032830	Pisum sativum	endo-1,4-beta-glucanase. EGL2.
AAC12684.1	U76725	Pinus radiata	endo-beta-1,4-glucanase. PrCell. cellulase; PRCEL1.
BAB32662.1	AB055886	Atriplex lentiformis	beta-1,4-glucanase. Al-cell. cellulase.
AAC62241.1	AF077339	Lycopersicon esculentum	endo-1,4-beta-glucanase. cel5. cellulase; also expressed in fruit and pistils.
CAA65826.1	X97188	Capsicum annuum	endo-beta-1,4-glucanase. ccell. cellulase.
AAA69909.1	U13055	Lycopersicon esculentum	cell wall hydrolase. endo-1,4-beta-glucanase precursor. Cel2. cellulase.
CAA65597.1	X96853	Prunus persica	endo-beta-1,4-glucanase. pcell.
CAA65600.1	X96856	Prunus persica	endo-beta-1,4-glucanase. ppEG1.
AAC12685.1	U76756	Pinus radiata	endo-beta-1,4-glucanase. PrCel2. cellulase; PRCEL2.
BAB39482.1	AB049199	Populus alba	endo-1,4-beta glucanase. PopCell1.
CAA65827.1	X97189	Capsicum annuum	endo-beta-1,4-glucanase. ccel3. cellulase.
BAB39483.1	AB049200	Populus alba	endo-1,4-beta-glucanase. PopCel2.
BAA77239.1	AB025796	Populus alba	endo-1,4-beta glucanase. POPCEL2. cellulase.
AAA69908.1	U13054	Lycopersicon esculentum	cell wall hydrolase. endo-1,4-beta-glucanase precursor. Cell. cellulase.

AAC78504.1	U34754	Phaseolus vulgaris	endo-1,4-beta-D-glucanase. cellulase.
AAA02563.1	M57400	Phaseolus vulgaris	cellulase precursor. endo-1,4-beta-D-glucanase.
CAA72133.1	Y11268	Lycopersicon esculentum	endo-1,4-beta-D-glucanase. cel7.
AAA96135.1	L41046	Pisum sativum	endo-1,4-beta-glucanase. EGL1.
CAB51903.1	AJ242807	Brassica napus	endo-1,4-beta-D-glucanase. Cell6. cellulase.
AAC49704.1	U78526	Lycopersicon esculentum	endo-1,4-beta-glucanase. Cel3.
BAA94257.1	AB040769	Hordeum vulgare	endo-1,4-beta-glucanase Cell1. Cell1.
CAA11302.1	AJ223387	Fragaria x ananassa	endo-beta-1,4-glucanase. partial cDNA obtained by RT-PCR amplification.
AAA20082.1	U00730	Glycine max	CMCase; cellulase; endo-1,4-beta-D-glucanase.
CAA11301.1	AJ223386	Fragaria x ananassa	endo-beta-1,4-glucanase. faEG1. partial cDNA obtained by RT-PCR amplification.
AAC64045.1	AF077340	Lycopersicon esculentum	endo-1,4-beta-glucanase. cel5. cellulase.
SEQ ID NO: 562			
AAD53011.1	AF089848	Brassica napus	senescence-specific cysteine protease. SAG12-1. BnSAG12-1.
AAD53012.1	AF089849	Brassica napus	senescence-specific cysteine protease. SAG12-2. BnSAG12-2.
AAK27968.1	AF242372	Ipomoea batatas	cysteine protease. SPCP1.
AAA50755.1	U13940	Alnus glutinosa	cysteine proteinase. putative preproprotein.
BAB13759.1	AB040454	Astragalus sinicus	cysteine proteinase. AsNODf32. preproprotein putative.
AAC62396.1	AF050756	Ricinus communis	cysteine endopeptidase precursor. CysEP.
CAB09698.1	Z97022	Hordeum vulgare	cysteine proteinase. putative.
CAA52425.1	X74406	Hemerocallis sp.	thiol-protease. SEN102.
BAA83472.1	AB004648	Oryza sativa	cysteine endopeptidase. RepA.

CAA56844.1	X80876	Oryza sativa	cysteine protease.
BAA88898.1	AB020961	Zea mays	cysteine protease component of protease-inhibitor complex. CPPIC.
AAC35211.1	U12637	Hemerocallis hybrid cultivar	cysteine proteinase. SEN11.
CAB09697.1	Z97021	Hordeum vulgare	cysteine endopeptidase EP-A. precursor.
AAB88263.1	AF019147	Zea mays	cysteine proteinase Mir3. mir3.
AAD28477.1	AF133839	Sandersonia aurantiaca	papain-like cysteine protease. PRT5. senescence-related.
CAB16317.1	Z99173	Nicotiana tabacum	storage protein hydrolysis. cysteine proteinase precursor.
CAB09699.1	Z97023	Hordeum vulgare	cysteine endopeptidase EP-A.
AAD10337.1	U94591	Hordeum vulgare	cysteine proteinase precursor. EPA.
CAA06243.1	AJ004958	Pisum sativum	thiol-protease. pre-pro-TPE4A protein. tpE4A.
CAB53515.1	AJ245924	Solanum tuberosum	proteolysis. cysteine protease. cyp.
AAD48496.1	AF172856	Lycopersicon esculentum	cysteine protease TDI-65. tdi-65. induced by drought; localized in the nuclei and chloroplast (Tabaeizadeh, Z. et al., 1995. Protoplasma, 186:208-219).
CAA05894.1	AJ003137	Lycopersicon esculentum	cysteine protease. CYP1. C14.
AAA79915.1	U17135	Dianthus caryophyllus	cysteine proteinase. DCCP1. expressed in senescing flower petals.
AAB37233.1	U34747	Phalaenopsis sp. SM9108	cysteine proteinase.
CAB17076.1	Z99954	Phaseolus vulgaris	protein hydrolysis. cysteine proteinase precursor.
CAA84378.1	Z34895	Vicia sativa	storage protein degradation. cysteine proteinase.
CAA53377.1	X75749	Vicia sativa	storage protein hydrolysis. cysteine protease.
CAB17074.1	Z99952	Phaseolus vulgaris	degradation of storage proteins. cysteine proteinase precursor.
AAB68374.1	U52970	Phaseolus vulgaris	suggested to initiate phaseolin degradation during germination. cysteine endopeptidase 1. PvCEP-1.

CAA12118.1 AJ224766 *Phaseolus vulgaris*
phaseolin degradation. cysteine protease.

AAC49455.1 U41902 *Pseudotsuga menziesii*
cysteine protease. Pseudotsain. PM33cysP.

CAA46863.1 X66061 *Pisum sativum*
thiolprotease. tpp. start codon ttg.

AAB41816.1 U44947 *Pisum sativum*
NTH1. PsCyp1. cysteine protease homolog.

BAA83473.1 AB004819 *Oryza sativa*
cysteine endopeptidase. Rep1.

BAA22544.1 D38532 *Ananas comosus*
precursor of cysteine proteinase. FBSB precursor. stem bromelain precursor in fruit.

BAA11170.1 D76415 *Oryza sativa*
cysteine proteinase.

AAD20453.1 AF099203 *Oryza sativa*
cysteine endopeptidase precursor. EP3A.

CAA08860.1 AJ009829 *Ananas comosus*
cysteine proteinase precursor, AN8. an8.

AAA85036.1 U19384 *Hordeum vulgare*
cysteine proteinase EPB2 precursor.

AAA85035.1 U19359 *Hordeum vulgare*
cysteine proteinase EPB1 precursor.

SEQ ID NO: 565

AAA97411.1 U51918 *Pisum sativum*
pyruvate dehydrogenase E1 alpha subunit.

CAA81558.1 Z26949 *Solanum tuberosum*
subunit of the mitochondrial pyruvate dehydrogenase complex. E1 alpha subunit of pyruvate dehydrogenase precursor.

AAC72195.1 AF069911 *Zea mays*
pyruvate dehydrogenase E1 alpha subunit.

AAG43499.1 AF209924 *Lycopersicon esculentum*
pyruvate dehydrogenase.

CAB08111.1 Z94180 *Lycopersicon esculentum*
branched chain alpha-keto acid dehydrogenase E1-alpha subunit.

SEQ ID NO: 566

AAD55090.1 AF178653 *Vitis riparia*
thaumatin. osmotin; pathogenesis-related protein.

CAA51432.1 X72928 *Solanum commersonii*
osmotin-like protein.

CAA47601.1 X67121 *Solanum commersonii*
osmotin-like protein.

CAC34055.1 AJ297410 *Capsicum annuum*
osmotin-like protein. pr5 p23.

CAA47047.1	X66416	Lycopersicon esculentum	tpm 1. Induced during viroid infection. Osmotin-like, antifungal protein homologue.
AAB23375.1	S44889	Nicotiana tabacum	osmotin. osmotin. pathogenesis-related protein homolog; This sequence comes from Fig. 3.
AAB22459.2	S40046	Nicotiana tabacum	osmotin. abscisic acid-activated. basic PR-like protein; This sequence comes from Fig. 1A; conceptual translation presented here differs from translation in publication; mismatch(181[R->G]).
AAG16625.1	AY007309	Solanum dulcamara	cryoprotective osmotin-like protein.
CAA46623.1	X65701	Nicotiana tabacum	osmotin. AP24.
CAA46622.1	X65700	Nicotiana tabacum	osmotin. AP24.
CAA51431.1	X72927	Solanum commersonii	osmotin-like protein.
CAA64620.1	X95308	Nicotiana tabacum	PR protein. osmotin.
CAA51430.1	X72926	Solanum commersonii	osmotin-like protein.
AAC64171.1	AF093743	Lycopersicon esculentum	pathogenesis-related protein osmotin precursor. NP24.
AAB61590.1	AF003007	Vitis vinifera	VVTL1. osmotin-like protein, PR-5 protein; thaumatin-like protein.
BAA11180.1	D76437	Nicotiana sylvestris	antifungal activity. neutral PR-5 (osmotin-like protein, PR-5d). neutral isoform of pathogenesis-related protein group 5.
AAA34087.1	M64081	Nicotiana tabacum	osmotin-like protein. OLP1.
CAA47669.1	X67244	Solanum commersonii	osmotin-like protein.
CAA71883.1	Y10992	Vitis vinifera	osmotin-like protein. OSM1.
AAF13707.1	AF199508	Fragaria x ananassa	osmotin-like protein. olp.
AAA34089.1	M29279	Nicotiana tabacum	osmotin.
CAA43854.1	X61679	Nicotiana tabacum	osmotin.
CAA04642.1	AJ001268	Hordeum vulgare	antifungal. basic pathogenesis-related protein PR5. osmotin/permatin-like.
CAC22330.1	AJ298304	Fagus sylvatica	stress protein. osmotin-like protein. olp2.

CAC22329.1 AJ298303 *Fagus sylvatica*
stress protein. osmotin-like protein. olp.

AAB67852.1 L76377 *Oryza sativa*
osmotin. 14b.

CAB36911.1 AJ000692 *Quercus suber*
stress protein. osmotin-like protein. olp.

SEQ ID NO: 569

BAA95814.1 AP002069 *Oryza sativa*
ESTs AU082579(S2069),D40238(S2069) correspond to a region of the predicted gene.
Similar to *Arabidopsis thaliana* vesicle-associated membrane protein 7C; synaptobrevin 7C.
(AF025332).

SEQ ID NO: 572

AAA92677.1 U13736 *Pisum sativum*
binds calcium. calmodulin-like protein.

AAA34015.1 L01433 *Glycine max*
calcium-binding regulatory protein. calmodulin. SCaM-4. putative.

AAA33948.1 L19359 *Glycine max*
calcium-binding regulatory protein. calmodulin. SCaM-5. putative.

CAA66159.1 X97558 *Capsicum annuum*
calmodulin-1.

CAA09302.1 AJ010645 *Capsicum annuum*
calcium binding protein. calmodulin 3 protein. calmodulin 3.

AAA34144.1 M67472 *Lycopersicon esculentum*
calmodulin. CALM1LE.

CAA62150.1 X90560 *Physcomitrella patens*
Calmodulin. CaM.

AAB46588.1 U83402 *Capsicum annuum*
calmodulin.

BAA87825.1 AP000815 *Oryza sativa*
ESTs AU030013(E50493),AU081341(E50493) correspond to a region of the predicted gene.
Similar to *O.sativa* gene encoding calmodulin. (Z12828).

AAF65511.1 AF108889 *Capsicum annuum*
calmodulin.

AAA85157.1 U20297 *Solanum tuberosum*
calcium-binding protein. calmodulin.

AAA85156.1 U20296 *Solanum tuberosum*
calcium-binding protein. calmodulin.

AAA62351.1 U20295 *Solanum tuberosum*
calcium-binding protein. calmodulin.

AAA85155.1 U20294 *Solanum tuberosum*
calcium-binding protein. calmodulin.

AAA33900.1 L18914 *Oryza sativa*
calcium binding protein, signal transduction. calmodulin.

CAA78288.1	Z12828	Oryza sativa	calcium binding protein, signal transduction. calmodulin.
AAC49583.1	U48692	Triticum aestivum	calmodulin TaCaM2-3. calcium-binding protein.
AAC49582.1	U48691	Triticum aestivum	calmodulin TaCaM2-2. calcium-binding protein.
CAA61980.1	X89890	Bidens pilosa	Calmodulin.
CAA67054.1	X98404	Capsicum annuum	calmodulin-2.
AAA33083.1	M20729	Chlamydomonas reinhardtii	calmodulin.
AAG11418.1	AF292108	Prunus avium	calmodulin.
AAF33852.1	AF231026	Oryza sativa	calmodulin-like protein.
AAA92681.1	U13882	Pisum sativum	calcium-binding protein. calmodulin.
AAA33706.1	M80836	Petunia x hybrida	calmodulin. CAM81.
AAA33705.1	M80831	Petunia x hybrida	calmodulin-related protein. CAM53.
AAA98933.1	U37936	Oryza sativa	novel calmodulin-like protein. C-terminal of this sequence contains a CAAX box which is common in signal transport protein, but not in calmodulin.
CAA43143.1	X60738	Malus x domestica	Calmodulin. CaM.
CAA78301.1	Z12839	Lilium longiflorum	calcium binding protein, signal transduction. calmodulin.
AAA33397.1	L18912	Lilium longiflorum	calcium binding protein, signal transduction. calmodulin. putative.
CAA42423.1	X59751	Daucus carota	calmodulin. Ccam-1.
AAF73157.1	AF150059	Brassica napus	calmodulin. CaM1. involved in seed germination.
AAA19571.1	U10150	Brassica napus	calcium binding. calmodulin. bcm1.
AAA87347.1	M88307	Brassica juncea	calmodulin.
AAG27432.1	AF295637	Elaeis guineensis	calmodulin.
BAA94697.1	AB041712	Chara corallina	calmodulin. cccam2.

BAA94696.1	AB041711	Chara corallina calmodulin. cccam1.
BAA96536.1	AB044286	Chara corallina calmodulin. ccam.
AAC18355.1	AF064456	Oryza sativa subsp. indica calmodulin-like protein. CAM-like.
AAA34237.1	L20691	Vigna radiata calmodulin.
CAA52602.1	X74490	Zea mays Calmodulin. ZMCALM1.
CAA54583.1	X77397	Zea mays calmodulin. CaM2.
AAC49585.1	U49103	Triticum aestivum calmodulin TaCaM3-2. calcium-binding protein.
AAC49586.1	U49104	Triticum aestivum calmodulin TaCaM3-3. calcium-binding protein.
AAC49587.1	U49105	Triticum aestivum calmodulin TaCaM4-1. calcium-binding protein.
AAC49580.1	U48689	Triticum aestivum calmodulin TaCaM1-3. calcium-binding protein.
AAC49584.1	U48693	Triticum aestivum calmodulin TaCaM3-1. calcium-binding protein.
SEQ ID NO: 575		
AAK28303.1	AF346431	Nicotiana tabacum phenylpropanoid:glucosyltransferase 1. togt1. glucosyltransferase.
AAB36653.1	U32644	Nicotiana tabacum immediate-early salicylate-induced glucosyltransferase. IS5a.
AAB36652.1	U32643	Nicotiana tabacum immediate-early salicylate-induced glucosyltransferase. IS10a.
AAK28304.1	AF346432	Nicotiana tabacum phenylpropanoid:glucosyltransferase 2. togt2. glucosyltransferase.
CAA59450.1	X85138	Lycopersicon esculentum twil. homologous to glucosyltransferases.
CAB56231.1	Y18871	Dorotheanthus bellidiformis betanidin-5-O-glucosyltransferase.
BAA83484.1	AB031274	Scutellaria baicalensis UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.
AAB48444.1	U82367	Solanum tuberosum UDP-glucose glucosyltransferase.
CAA54610.1	X77460	Manihot esculenta UTP-glucose glucosyltransferase. CGT4.

AAD04166.1	AF101972	Phaseolus lunatus	catalyzes formation of O-glucosylzeatin from zeatin and UDPG; catalyzes formation of O-xylosylzeatin from zeatin and UDPX. zeatin O-glucosyltransferase. ZOG1. cytokinin O-glucosyltransferase.
BAB17182.1	AP002843	Oryza sativa	putative UTP-glucose glucosyltransferase. P0407B12.19.
BAA93039.1	AB033758	Citrus unshiu	limonoid UDP-glucosyltransferase. LGTase.
AAF61647.1	AF190634	Nicotiana tabacum	UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.
BAB17176.1	AP002843	Oryza sativa	putative UTP-glucose glucosyltransferase. P0407B12.13.
CAC09351.1	AL442007	Oryza sativa	putative glucosyltransferase. H0212B02.7.
CAA54611.1	X77461	Manihot esculenta	UTP-glucose glucosyltransferase. CGT2.
AAF98390.1	AF287143	Brassica napus	catalyzes the transfer of glucose from UDP-glucose to sinapate and some other hydroxycinnamates (4-coumarate, caffeate, ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.
AAK16181.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.16.
AAK16178.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.5.
CAA54612.1	X77462	Manihot esculenta	UTP-glucose glucosyltransferase. CGT5.
AAK16180.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.21.
AAF17077.1	AF199453	Sorghum bicolor	UDP-glucose glucosyltransferase. UDP-glucose:p-hydroxymandelonitrile-o-glucosyltransferase.
CAA54609.1	X77459	Manihot esculenta	UTP-glucose glucosyltransferase. CGT1.
BAB41025.1	AB047098	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. FlUFGT1.
AAK16172.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.14.
BAB41019.1	AB047092	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT1.
BAB41018.1	AB047091	Vitis labrusca x Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT2. The gene originated in one of the parents V. vinifera cv. Centennial.

BAB41023.1	AB047096	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT1.
BAB41021.1	AB047094	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT1.
BAA89009.1	AB027455	Petunia x hybrida	anthocyanin 5-O-glucosyltransferase. PH1.
AAB81682.1	AF000371	Vitis vinifera	UDP glucose:flavonoid 3-o-glucosyltransferase.
BAB41017.1	AB047090	Vitis labrusca x Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT1. The gene was derived from one of the parents V. labruscana cv. Ishiharawase.
BAB41022.1	AB047095	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT2.
BAB41020.1	AB047093	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT2.
BAB41024.1	AB047097	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT2.
AAB81683.1	AF000372	Vitis vinifera	UDP glucose:flavonoid 3-o-glucosyltransferase.
BAB41026.1	AB047099	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT2.
CAA54613.1	X77463	Manihot esculenta	UTP-glucose glucosyltransferase. CGT6.
BAA89008.1	AB027454	Petunia x hybrida	anthocyanidin 3-O-glucosyltransferase. PGT8.
BAA12737.1	D85186	Gentiana triflora	UDP-glucose:flavonoid-3-glucosyltransferase.
SEQ ID NO: 576			
CAB60277.1	AJ002586	Solanum tuberosum	UCP.
CAA72107.1	Y11220	Solanum tuberosum	mitochondrial uncoupling protein.
BAA92172.1	AB024733	Symplocarpus renifolius	SfUCPa. SfUCPa.
BAB40658.1	AB049998	Oryza sativa	uncoupling protein. OsUCP2.
BAA92173.1	AB024734	Symplocarpus renifolius	SfUCPb. SfUCPb.
BAB16385.1	AB042429	Triticum aestivum	uncoupling protein. WhUCP1b.
BAB16384.1	AB042428	Triticum aestivum	uncoupling protein. WhUCP1a.

BAB40657.1 AB049997 *Oryza sativa*
uncoupling protein. OsUCP1.

SEQ ID NO: 577

AAA19571.1 U10150 *Brassica napus*
calcium binding. calmodulin. bcm1.

AAA87347.1 M88307 *Brassica juncea*
calmodulin.

AAA92681.1 U13882 *Pisum sativum*
calcium-binding protein. calmodulin.

AAA33706.1 M80836 *Petunia x hybrida*
calmodulin. CAM81.

CAA43143.1 X60738 *Malus x domestica*
Calmodulin. CaM.

CAA78301.1 Z12839 *Lilium longiflorum*
calcium binding protein, signal transduction. calmodulin.

AAA33397.1 L18912 *Lilium longiflorum*
calcium binding protein, signal transduction. calmodulin. putative.

CAA42423.1 X59751 *Daucus carota*
calmodulin. Ccam-1.

AAG27432.1 AF295637 *Elaeis guineensis*
calmodulin.

AAG11418.1 AF292108 *Prunus avium*
calmodulin.

AAA34237.1 L20691 *Vigna radiata*
calmodulin.

AAC49587.1 U49105 *Triticum aestivum*
calmodulin TaCaM4-1. calcium-binding protein.

AAC49586.1 U49104 *Triticum aestivum*
calmodulin TaCaM3-3. calcium-binding protein.

AAC49585.1 U49103 *Triticum aestivum*
calmodulin TaCaM3-2. calcium-binding protein.

AAC49584.1 U48693 *Triticum aestivum*
calmodulin TaCaM3-1. calcium-binding protein.

AAC49580.1 U48689 *Triticum aestivum*
calmodulin TaCaM1-3. calcium-binding protein.

AAC49579.1 U48688 *Triticum aestivum*
calmodulin TaCaM1-2. calcium binding protein.

AAC49578.1 U48242 *Triticum aestivum*
calmodulin TaCaM1-1. calcium-binding.

AAA03580.1 L01431 *Glycine max*
calcium-binding regulatory protein. calmodulin. SCaM-2. putative.

AAB36130.1	S81594	Vigna radiata	auxin-regulated calmodulin. auxin-regulated calmodulin, arCaM. This sequence comes from Fig. 1; arCaM.
AAA33901.1	L18913	Oryza sativa	calcium binding protein, signal transduction. calmodulin. putative.
CAA78287.1	Z12827	Oryza sativa	calcium binding protein, signal transduction. calmodulin.
AAB46588.1	U83402	Capsicum annuum	calmodulin.
AAA32938.1	M27303	Hordeum vulgare	calmodulin.
BAA88540.1	AP000969	Oryza sativa	ESTs AU081349(E61253), D41425(S3918) correspond to a region of the predicted gene. Similar to calmodulin. (AF042840).
AAF65511.1	AF108889	Capsicum annuum	calmodulin.
AAC36059.1	AF042840	Oryza sativa	calmodulin. CaM1.
AAA34238.1	L20507	Vigna radiata	calmodulin.
AAA34014.1	L01432	Glycine max	calcium-binding regulatory protein. calmodulin. SCaM-3. putative.
AAA34013.1	L01430	Glycine max	calcium-binding regulatory protein. calmodulin. SCaM-1. putative.
CAA36644.1	X52398	Medicago sativa	calmodulin (AA 1-149).
AAB68399.1	U79736	Helianthus annuus	calmodulin. HaCaM.
AAD10244.1	AF030032	Phaseolus vulgaris	calmodulin. CaM. EF-hand protein; calcium-dependent protein; functions in calcium signal transduction pathways.
AAA33705.1	M80831	Petunia x hybrida	calmodulin-related protein. CAM53.
AAA16320.1	L14071	Bryonia dioica	calmodulin. Bc329. calcium-binding sites (amino acid #): 1. (21..33); 2. (57..68); 3. (94..106); 4. (130..141).
CAA61980.1	X89890	Bidens pilosa	Calmodulin.
AAA33900.1	L18914	Oryza sativa	calcium binding protein, signal transduction. calmodulin.
CAA78288.1	Z12828	Oryza sativa	calcium binding protein, signal transduction. calmodulin.

CAA74307.1	Y13974	Zea mays	calmodulin.
AAC49583.1	U48692	Triticum aestivum	calmodulin TaCaM2-3. calcium-binding protein.
AAC49582.1	U48691	Triticum aestivum	calmodulin TaCaM2-2. calcium-binding protein.
AAA85157.1	U20297	Solanum tuberosum	calcium-binding protein. calmodulin.
AAA85156.1	U20296	Solanum tuberosum	calcium-binding protein. calmodulin.
AAA62351.1	U20295	Solanum tuberosum	calcium-binding protein. calmodulin.
AAA85155.1	U20294	Solanum tuberosum	calcium-binding protein. calmodulin.
CAA46150.1	X65016	Oryza sativa	calmodulin. cam.
AAD10246.1	AF030034	Phaseolus vulgaris	calmodulin. CaM. EF-hand protein; calcium-dependent protein; functions in calcium signal transduction pathways.
AAF73157.1	AF150059	Brassica napus	calmodulin. CaM1. involved in seed germination.
CAA54583.1	X77397	Zea mays	calmodulin. CaM2.
SEQ ID NO: 578			
AAF01764.2	AF184277	Glycine max	homeodomain-leucine zipper protein 56. Hdl56. transcription factor.
BAA21017.1	D26578	Daucus carota	transcriptional regulator. DNA-binding protein. homeodomain at nt 761-940; leucine zipper at nt 941-1048.
AAD37697.1	AF145728	Oryza sativa	homeodomain leucine zipper protein. Oshox4. transcription factor.
CAB67118.1	Y17306	Lycopersicon esculentum	homeodomain protein. h52.
AAF01765.1	AF184278	Glycine max	homeodomain-leucine zipper protein 57. Hdl57. transcription factor.
BAA05624.1	D26575	Daucus carota	transcriptional regulator. DNA-binding protein. homeodomain at nt 520-699; leucine zipper at nt 700-805.
BAA93466.1	AB028078	Physcomitrella patens	homeobox protein PpHB7. PpHB7. homeodomain-leucine zipper gene.
BAA93465.1	AB028077	Physcomitrella patens	homeobox protein PpHB6. PpHB6. homeodomain-leucine zipper gene.

BAA93464.1	AB028076	Physcomitrella patens	homeobox protein PpHB5. PpHB5. homeodomain-leucine zipper gene.
BAA05622.1	D26573	Daucus carota	transcriptional regulator. DNA-binding protein. homeodomain at nt 585-764; leucine zipper at nt 765-851.
BAA05625.1	D26576	Daucus carota	transcriptional regulator. DNA-binding protein. homeodomain at nt 300-479; leucine zipper at nt 480-587.
BAA05623.1	D26574	Daucus carota	transcriptional regulator. DNA-binding protein. homeodomain at nt 498-677; leucine zipper at nt 678-785.
AAD37698.1	AF145729	Oryza sativa	homeodomain leucine zipper protein. Oshox5. transcription factor.
BAA93461.1	AB028073	Physcomitrella patens	homeobox protein PpHB2. PpHB2. homeodomain-leucine zipper gene.
BAA93467.1	AB028079	Physcomitrella patens	homeobox protein PpHB8. PpHB8. homeodomain-leucine zipper gene.
BAA93468.1	AB028080	Physcomitrella patens	homeobox protein PpHB9. PpHB9. homeodomain-leucine zipper gene.
BAA93460.1	AB028072	Physcomitrella patens	homeobox protein PpHB1. PpHB1. homeodomain-leucine zipper gene.
AAD37699.1	AF145730	Oryza sativa	homeodomain leucine zipper protein. Oshox6. transcription factor.
CAA06717.1	AJ005820	Craterostigma plantagineum	transcription factor. homeodomain leucine zipper protein. hb-1.
BAA93463.1	AB028075	Physcomitrella patens	homeobox protein PpHB4. PpHB4. homeodomain-leucine zipper gene.
CAA65456.2	X96681	Oryza sativa	transcription factor. DNA-binding protein. Oshox1. homeodomain leucine zipper gene.
AAF19980.1	AF211193	Oryza sativa	homeodomain-leucine zipper transcription factor. Hox1. hox1.
AAK31270.1	AC079890	Oryza sativa	homeodomain leucine zipper protein hox1. OSJNBb0089A17.12.
CAA06728.1	AJ005833	Craterostigma plantagineum	transcription factor. homeodomain leucine zipper protein. hb-2.
AAD37696.1	AF145727	Oryza sativa	homeodomain leucine zipper protein. Oshox3. transcription factor.
SEQ ID NO: 580			
AAD32141.1	AF123503	Nicotiana tabacum	Nt-gh3 deduced protein.
CAA42636.1	X60033	Glycine max	auxin-responsive GH3 product. GH3.

BAA96221.1 AP002094 *Oryza sativa*

ESTs C19814(E10971), AU090481(E10971) correspond to a region of the predicted gene. Similar to *Arabidopsis thaliana* chromosome 2, sequence from clones T3F17, F11C10, F13A10; auxin-responsive GH3-like protein (AC006526).

SEQ ID NO: 581

AAD13632.1 AF059488 *Lycopersicon esculentum*
expansin precursor. Exp4.

AAF32410.1 AF230277 *Triphysaria versicolor*
alpha-expansin 2.

CAA04385.1 AJ000885 *Brassica napus*
Cell wall extension in plants. Expansin.

CAB46492.1 AJ243340 *Lycopersicon esculentum*
expansin9. exp9.

AAC63088.1 U82123 *Lycopersicon esculentum*
expansin. LeEXP1. fruit ripening regulated expansin.

CAA06271.2 AJ004997 *Lycopersicon esculentum*
expansin18. exp18.

AAF62182.1 AF247164 *Oryza sativa*
alpha-expansin OsEXP7. cell wall loosening factor; expressed in internodes and leaves.

AAF35900.1 AF230331 *Zinnia elegans*
expansin. Exp1.

AAG13982.1 AF297521 *Prunus avium*
expansin 1. Exp1. PruavExp1.

AAC33529.1 U93167 *Prunus armeniaca*
expansin. PA-Exp1.

AAF21101.1 AF159563 *Fragaria x ananassa*
expansin. Exp2. ripening regulated.

AAF35901.1 AF230332 *Zinnia elegans*
expansin 2.

AAG13983.1 AF297522 *Prunus avium*
expansin 2. Exp2. PruavExp2.

AAC33530.1 AF038815 *Prunus armeniaca*
expansin. Exp2.

BAB19676.1 AB029083 *Prunus persica*
expansin. PchExp1.

AAB40637.1 U64893 *Pinus taeda*
expansin. similar to *Arabidopsis* expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to *Cucumis sativus* expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.

AAB37746.1 U30382 *Cucumis sativus*
expansin S1 precursor. Cs-EXP1. similar to pollen allergen Lol pI, *Lolium perenne*, Swiss-Prot Accession Number P14946; former gene name CuExS1; expansin-29 (Ex29) protein.

CAC19184.1	AJ291817	Cicer arietinum	expansin.
AAD47901.1	AF085330	Pinus taeda	expansin.
AAB40634.1	U64890	Pinus taeda	expansin. similar to Arabidopsis expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to Cucumis sativus expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.
AAF32409.1	AF230276	Triphysaria versicolor	alpha-expansin 3.
AAC39512.1	AF043284	Gossypium hirsutum	expansin. GhEX1. contains N-terminal signal peptide.
AAB40635.1	U64891	Pinus taeda	expansin. similar to Arabidopsis expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to Cucumis sativus expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.
AAC96081.1	AF049354	Nicotiana tabacum	involved in acid-growth response. alpha-expansin precursor. Nt-EXP5. cell wall protein.
AAB38074.1	U30477	Oryza sativa	induces extension (creep) in plant cell walls. expansin Os-EXP2. Os-EXP2. former gene name RiExB.
AAG32921.1	AF184233	Lycopersicon esculentum	expansin. Exp10.
AAB81662.1	U85246	Oryza sativa	expansin. Os-EXP4.
AAD49956.1	AF167360	Rumex palustris	expansin. EXP1.
AAB40636.1	U64892	Pinus taeda	expansin. similar to Arabidopsis expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to Cucumis sativus expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.
AAF32411.1	AF230278	Triphysaria versicolor	alpha-expansin 1.
AAC96080.1	AF049353	Nicotiana tabacum	involved in acid-growth response. alpha-expansin precursor. Nt-EXP4. cell wall protein.
AAF35902.1	AF230333	Zinnia elegans	expansin 3.
CAB43197.1	AJ239068	Lycopersicon esculentum	cell wall loosening enzyme. expansin2. exp2.
AAC64201.1	AF096776	Lycopersicon esculentum	expansin. LeEXP2.

AAF17570.1	AF202119	Marsilea quadrifolia	alpha-expansin. EXP1. Mq-EXP1.
AAD13633.1	AF059489	Lycopersicon esculentum	expansin precursor. Exp5.
AAF62181.1	AF247163	Oryza sativa	alpha-expansin OsEXP6. cell wall loosening factor; expressed in internodes and leaves.
AAF17571.1	AF202120	Regnellidium diphyllum	alpha-expansin. EXP1. Rd-EXP1.
AAF62180.1	AF247162	Oryza sativa	alpha-expansin OsEXP5. cell wall loosening factor; expressed in internodes, leaves, coleoptiles, and roots.
CAC19183.1	AJ291816	Cicer arietinum	expansin.
CAC06433.1	AJ276007	Festuca pratensis	expansin. exp2.
BAB32732.1	AB049406	Eustoma grandiflorum	expansin. Eg Expansin.
AAG01875.1	AF291659	Striga asiatica	alpha-expansin 3. Exp3.
AAB37749.1	U30460	Cucumis sativus	expansin S2 precursor. Cs-EXP2. similar to pollen allergen Lol pI, Lolium perenne, Swiss-Prot Accession Number P14946; former gene name CuExS2; expansin-30 (Ex30) protein.
AAC96077.1	AF049350	Nicotiana tabacum	involved in acid-growth response. alpha-expansin precursor. Nt-EXP1. cell wall protein.
AAC96079.1	AF049352	Nicotiana tabacum	involved in acid-growth response. alpha-expansin precursor. Nt-EXP3. cell wall protein.
AAG32920.1	AF184232	Lycopersicon esculentum	expansin. Exp8.
CAA69105.1	Y07782	Oryza sativa	expansin. RiExA.
AAC96078.1	AF049351	Nicotiana tabacum	involved in acid-growth response. alpha-expansin precursor. Nt-EXP2. cell wall protein.
SEQ ID NO: 583			
BAA85412.1	AP000615	Oryza sativa	ESTs AU065232(E60855), C23624(S1554), AU078241(E60855) correspond to a region of the predicted gene.; similar to putative adenylate kinase. (AC005896).
BAA01181.1	D10335	Oryza sativa	adenylate kinase-b. Adk-b.
BAA01180.1	D10334	Oryza sativa	adenylate kinase-a. Adk-a.
BAA94761.1	AB041773	Oryza sativa	adenylate kinase. Adk-a.

AAB68604.1 U82330 *Prunus armeniaca*
adenylate kinase homolog.

AAF23372.1 AF187063 *Oryza sativa*
catalyzes the transfer of phosphate from ATP to UMP or CMP to form ADP and UDP or CDP. UMP/CMP kinase b. *ura6*.

AAF23371.1 AF187062 *Oryza sativa*
catalyzes the transfer of phosphate from ATP to UMP or CMP to form ADP and UDP or CDP. UMP/CMP kinase a. *ura6*.

AAD41679.1 AF086603 *Ceratopteris richardii*
adenylate kinase. ADK1.

BAA85443.1 AP000616 *Oryza sativa*
similar to UMP/CMP kinase (AF000147).

SEQ ID NO: 584

BAA87052.2 D88273 *Hordeum vulgare*
nicotianamine aminotransferase A. *naat-A*.

BAA87055.1 AB024006 *Hordeum vulgare*
nicotianamine aminotransferase. *naat-A*.

BAA87053.1 AB005788 *Hordeum vulgare*
nicotianamine aminotransferase B. *naat-b*. NAAT-B.

BAA87054.1 AB024006 *Hordeum vulgare*
nicotianamine aminotransferase. *naat-B*.

BAA77261.1 AB007405 *Oryza sativa*
alanine aminotransferase. *AlaAT*.

BAA77260.1 AB007404 *Oryza sativa*
alanine aminotransferase. *AlaAT*.

CAA49199.1 X69421 *Panicum miliaceum*
alanine aminotransferase. *pAlaAT-2*.

AAB01685.1 U31975 *Chlamydomonas reinhardtii*
catalyzes the transfer of -NH₂ from ala to 2-oxoglutarate. alanine aminotransferase. The translation start site has not been experimentally tested, but a 55 kDa product can be detected in Western blot.

AAC62456.1 AF055898 *Zea mays*
alanine aminotransferase. *alt. AlaAT*.

CAA81231.1 Z26322 *Hordeum vulgare*
alanine aminotransferase.

SEQ ID NO: 586

AAB94589.1 AF022460 *Glycine max*
CYP83D1p. CYP83D1. cytochrome P450 monooxygenase.

AAA32913.1 M32885 *Persea americana*
cytochrome P-450LXXIA1 (*cyp71A1*).

AAA19701.1 L24438 *Thlaspi arvense*
cytochrome P450.

BAB40324.1	AB037245	Asparagus officinalis cytochrome P450. ASPI-2.
AAC39318.1	AF029858	Sorghum bicolor second multifunctional cytochrome P450 in the biosynthetic pathway of the cyanogenic glucoside dhuririn. Catalyzes the conversion of p-hydroxyphenylacetaldoxime to p- hydroxymandelonitrile. cytochrome P450 CYP71E1. CYP71E1. No EST#s identified.
BAB40323.1	AB037244	Asparagus officinalis cytochrome P450. ASPI-1.
CAA71517.1	Y10493	Glycine max putative cytochrome P450.
AAB61965.1	U48435	Solanum chacoense putative cytochrome P450.
CAA70575.1	Y09423	Nepeta racemosa cytochrome P450. CYP71A5.
CAA71513.1	Y10489	Glycine max putative cytochrome P450.
AAB61964.1	U48434	Solanum chacoense putative cytochrome P450.
AAD47832.1	AF166332	Nicotiana tabacum cytochrome P450.
AAB94588.1	AF022459	Glycine max CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.
AAF27282.1	AF122821	Capsicum annuum cytochrome P450. PepCYP.
CAA50312.1	X70981	Solanum melongena P450 hydroxylase. CYPEG2.
CAA83941.1	Z33875	Mentha x piperita cytochrome P-450 oxidase.
AAG44132.1	AF218296	Pisum sativum cytochrome P450. P450 isolog.
CAA70576.1	Y09424	Nepeta racemosa cytochrome P450. CYP71A6.
AAD44151.1	AF124816	Mentha x piperita cytochrome p450 isoform PM17.
BAA03635.1	D14990	Solanum melongena Cytochrome P-450EG4.
CAA50645.1	X71654	Solanum melongena P450 hydroxylase.
AAB69644.1	AF000403	Lotus japonicus putative cytochrome P450. LjNP450.
AAD37433.1	AF150881	Lycopersicon esculentum x Lycopersicon peruvianum catalyzes the hydroxylation of ferulic acid to 5-hydroxyferulic acid. ferulate-5-hydroxylase. CYP84. cytochrome P450-dependent monooxygenase; F5H; FAH1.

CAA65580.1	X96784	Nicotiana tabacum	cytochrome P450. hsr515.
AAD44152.1	AF124817	Mentha x piperita	cytochrome p450 isoform PM2.
CAA64635.1	X95342	Nicotiana tabacum	cytochrome P450. hsr515. hypersensitivity-related gene.
AAG14962.1	AF214008	Brassica napus	cytochrome p450-dependent monooxygenase. BNF5H2.
AAG14961.1	AF214007	Brassica napus	cytochrome p450-dependent monooxygenase. BNF5H1.
CAB56503.1	AJ238612	Catharanthus roseus	cytochrome P450.
AAG14963.1	AF214009	Brassica napus	cytochrome p450-dependent monooxygenase. BNF5H3.
AAK38088.1	AF321864	Lolium rigidum	putative cytochrome P450.
AAD44150.1	AF124815	Mentha spicata	cytochrome p450.
AAK38084.1	AF321860	Lolium rigidum	putative cytochrome P450.
AAD56282.1	AF155332	Petunia x hybrida	flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.
AAK38087.1	AF321863	Lolium rigidum	putative cytochrome P450.
AAK38083.1	AF321859	Lolium rigidum	putative cytochrome P450.
AAB94584.1	AF022157	Glycine max	capable of catalyzing the metabolism of phenylurea herbicides. CYP71A10. CYP71A10. cytochrome P450 monooxygenase.
CAA71514.1	Y10490	Glycine max	putative cytochrome P450.
BAA12159.1	D83968	Glycine max	Cytochrome P-450 (CYP93A1).
BAB39252.1	AP002968	Oryza sativa	putative cytochrome P450. P0416G11.1.
CAA50155.1	X70824	Solanum melongena	flavonoid hydroxylase (P450). CYP75.

SEQ ID NO: 587

CAA60120.1	X86222	Pisum sativum	heat shock protein. hsp22.
AAF37726.1	AF237957	Euphorbia esula	LMW heat shock protein. putative 22 kDa mitochondrial heat shock protein.

BAA32547.1	AB017134	Lycopersicon esculentum mitochondrial small heat shock protein. LEMTSHP.
CAA33388.1	X15333	Chenopodium rubrum heat shock protein (AA 1-204).
AAB03096.1	U21722	Glycine max Hsp23.9. Gmhs23.9. low molecular weight heat shock protein.
AAC12279.1	AF035460	Zea mays low molecular weight heat shock protein precursor. hsp22.
AAD03604.1	AF104107	Triticum aestivum small heat shock protein Hsp23.5. mRNA not present, or only at very low levels, prior to heat stress; mRNA abundant after two hours at 40C.
AAB01557.1	L47741	Picea glauca mitochondria-localized low molecular weight heat shock protein 23.5. EMB22, SMW HSP23.5.
AAD03605.1	AF104108	Triticum aestivum small heat shock protein Hsp23.6.
CAA38037.1	X54103	Plastid Petunia x hybrida heat shock protein. hsp21.
AAF19022.1	AF197942	Funaria hygrometrica chloroplast-localized small heat shock protein 22. CPsHSP22.
AAB49626.1	U59917	Lycopersicon esculentum chromoplast-associated hsp20. pTOM111. small molecular weight heat shock protein.
AAB07023.1	U66300	Chloroplast Lycopersicon esculentum heat shock protein. HSP21.
BAA29064.1	D88584	Nicotiana tabacum heat shock protein 26 (Type I). Nthsp26a. plastid-localized small heat shock protein.
AAF19021.1	AF197941	Funaria hygrometrica chloroplast-localized small heat shock protein. CPsHSP21. CPsHS 21.
BAA78385.1	AB020973	Oryza sativa heat shock protein 26. Oshsp26. chloroplast-localized small heat shock protein.
CAA41219.1	X58280	Triticum aestivum heat shock protein 26.6. Tahsp26.6.
AAC96315.1	AF097657	Triticum aestivum heat shock protein HSP26. hsp26.6. similar to the Triticum aestivum hsp26.6G2 protein encoded by the sequence presented in GenBank Accession Number L41503; 26 kDa protein.
AAC96316.1	AF097658	Triticum aestivum heat shock protein HSP26. hsp26.6. 26 kDa protein.
AAC96314.1	AF097656	Triticum aestivum heat shock protein HSP26. hsp26.6. 26 kDa protein.
CAA47745.1	X67328	Triticum aestivum heat shock protein 26.6B. hsp 26.6B.
AAC96317.1	AF097659	Triticum aestivum heat shock protein HSP26. hsp26.6. 26 kDa protein.

AAA33477.1	L28712	<i>Zea mays</i>	heat shock protein 26. HSP26. plastid-localized low molecular weight hsp.
BAA29066.1	AB006043	<i>Nicotiana sylvestris</i>	heat shock protein 26. hsp26. plastid-localized small heat shock protein.
BAA29067.1	AB006044	<i>Nicotiana tomentosiformis</i>	heat shock protein 26. hsp26. plastid-localized small heat shock protein.
BAA29065.1	AB006041	<i>Nicotiana tabacum</i>	heat shock protein 26 (Type I). Nthsp26a. plastid-localized small heat shock protein 26.
AAC01570.1	AF019144	<i>Agrostis stolonifera</i> var. <i>palustris</i>	low molecular weight heat shock protein.
AAD30452.1	AF123255	<i>Lycopersicon esculentum</i>	17.7 kD class I small heat shock protein. HSP17.7.
CAA39603.1	X56138	<i>Lycopersicon esculentum</i>	small heat shock protein (class I).
AAD30453.1	AF123256	<i>Lycopersicon esculentum</i>	17.8 kD class I small heat shock protein. HSP17.8.
AAD30454.1	AF123257	<i>Lycopersicon esculentum</i>	17.6 kD class I small heat shock protein. HSP17.6.
AAD49336.1	AF166277	<i>Nicotiana tabacum</i>	low molecular weight heat-shock protein. LHS-1. TLHS-1.
AAF34133.1	AF161179	<i>Malus x domestica</i>	low molecular weight heat shock protein. Hsp1.
AAC39360.1	U63631	<i>Fragaria x ananassa</i>	LMW heat shock protein.
AAA61632.1	U08601	<i>Papaver somniferum</i>	low molecular weight heat-shock protein.
CAA08908.1	AJ009880	<i>Castanea sativa</i>	molecular chaperone. cytosolic class I small heat-shock protein HSP17.5. hsp17.5.
AAA33975.1	M11395	<i>Glycine max</i>	small heat shock protein.
CAA63570.1	X92983	<i>Pseudotsuga menziesii</i>	low molecular weight heat-shock protein.
AAB03893.1	M11318	<i>Glycine max</i>	17.5 kd heat shock protein Gmhsp17.6L.
CAA25578.1	X01104	<i>Glycine max</i>	heat shock protein 6871 (aa 1-153).
AAB72109.1	AF022217	<i>Brassica rapa</i>	low molecular weight heat-shock protein. BcHSP17.6. 17.6 kDa; cytosolic class I.
CAA46641.1	X65725	<i>Zea mays</i>	heat shock protein 17.2. Zmhsp 17.2. Class I low molecular weight heat shock protein.
CAB08441.1	Z95153	<i>Helianthus annuus</i>	17.6 kD class I small heat-shock protein HSP17.6. Ha hsp17.6.

AAA33974.1 M11317 Glycine max
17.6 kd heat shock protein Gmhsp17.6L.

SEQ ID NO: 588

AAA32913.1 M32885 Persea americana
cytochrome P-450LXXIA1 (cyp71A1).

AAA19701.1 L24438 Thlaspi arvense
cytochrome P450.

AAC39318.1 AF029858 Sorghum bicolor
second multifunctional cytochrome P450 in the biosynthetic pathway of the cyanogenic
glucoside dhurrin. Catalyzes the conversion of p-hydroxyphenylacetaldoxime to p-
hydroxymandelonitrile. cytochrome P450 CYP71E1. CYP71E1. No EST#s identified.

BAB40323.1 AB037244 Asparagus officinalis
cytochrome P450. ASPI-1.

BAB40324.1 AB037245 Asparagus officinalis
cytochrome P450. ASPI-2.

AAB94589.1 AF022460 Glycine max
CYP83D1p. CYP83D1. cytochrome P450 monooxygenase.

CAA71513.1 Y10489 Glycine max
putative cytochrome P450.

CAA70575.1 Y09423 Nepeta racemosa
cytochrome P450. CYP71A5.

AAB94584.1 AF022157 Glycine max
capable of catalyzing the metabolism of phenylurea herbicides. CYP71A10. CYP71A10.
cytochrome P450 monooxygenase.

AAB61965.1 U48435 Solanum chacoense
putative cytochrome P450.

AAF27282.1 AF122821 Capsicum annuum
cytochrome P450. PepCYP.

CAB56503.1 AJ238612 Catharanthus roseus
cytochrome P450.

AAD47832.1 AF166332 Nicotiana tabacum
cytochrome P450.

AAB94588.1 AF022459 Glycine max
CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.

AAB61964.1 U48434 Solanum chacoense
putative cytochrome P450.

CAA71517.1 Y10493 Glycine max
putative cytochrome P450.

CAA50645.1 X71654 Solanum melongena
P450 hydroxylase.

BAA03635.1 D14990 Solanum melongena
Cytochrome P-450EG4.

CAA50312.1	X70981	Solanum melongena	P450 hydroxylase. CYPEG2.
CAA71514.1	Y10490	Glycine max	putative cytochrome P450.
AAB69644.1	AF000403	Lotus japonicus	putative cytochrome P450. LjNP450.
CAA70576.1	Y09424	Nepeta racemosa	cytochrome P450. CYP71A6.
AAD44151.1	AF124816	Mentha x piperita	cytochrome p450 isoform PM17.
AAK38084.1	AF321860	Lolium rigidum	putative cytochrome P450.
CAA83941.1	Z33875	Mentha x piperita	cytochrome P-450 oxidase.
AAK38083.1	AF321859	Lolium rigidum	putative cytochrome P450.
AAD44152.1	AF124817	Mentha x piperita	cytochrome p450 isoform PM2.
BAB39252.1	AP002968	Oryza sativa	putative cytochrome P450. P0416G11.1.
AAD44150.1	AF124815	Mentha spicata	cytochrome p450.
AAK38087.1	AF321863	Lolium rigidum	putative cytochrome P450.
AAK38082.1	AF321858	Lolium rigidum	putative cytochrome P450.
CAA57423.1	X81829	Zea mays	cytochrome P450. CYP71C2. family CYP71, subfamily CYP71C.
CAA72208.1	Y11404	Zea mays	cytochrome p450. cyp71c2.
CAC27827.1	AJ295719	Catharanthus roseus	geraniol hydroxylase. cytochrome P450. cyp71.
AAG44132.1	AF218296	Pisum sativum	cytochrome P450. P450 isolog.
AAK38088.1	AF321864	Lolium rigidum	putative cytochrome P450.
AAG14963.1	AF214009	Brassica napus	cytochrome p450-dependent monooxygenase. BNF5H3.
CAA57424.2	X81830	Zea mays	cytochrome P450. CYP71C3. family CYP71, subfamily CYP71C.
CAA72207.1	Y11403	Zea mays	cytochrome p450. cyp71c3.

AAG14962.1 AF214008 Brassica napus
cytochrome p450-dependent monooxygenase. BNF5H2.

AAG14961.1 AF214007 Brassica napus
cytochrome p450-dependent monooxygenase. BNF5H1.

BAA12159.1 D83968 Glycine max
Cytochrome P-450 (CYP93A1).

BAB40322.1 AB036772 Triticum aestivum
cytochrome P450. N-1.

SEQ ID NO: 593

BAA09645.1 D63331 Nicotiana tabacum
Indole-3-acetonitrile hydrolysis. nitrilase. TNIT4. Indole-3-acetonitrile hydrolysis, indole-3-acetic acid biosynthesis.

BAA11770.1 D83078 Nicotiana tabacum
indole-3-acetonitrile hydrolysis. nitrilase. TNIT4B. indole-3-acetonitrile hydrolysis, indole-3-acetic acid biosynthesis.

BAA77679.1 AB027054 Oryza sativa
nitrilase-like protein. ONIT4.

SEQ ID NO: 595

AAG01147.1 AF283816 Pinus taeda
calreticulin. calcium-binding protein.

CAA05161.1 AJ002057 Beta vulgaris
calreticulin.

AAB71419.1 U74630 Ricinus communis
calreticulin.

AAB71420.1 U74631 Ricinus communis
endoplasmic reticulum calcium binding protein. calreticulin.

CAA95999.1 Z71395 Nicotiana glauca
ER Ca²⁺ binding protein. calreticulin. cal1.

AAD17490.1 AF052040 Berberis stolonifera
possible molecular chaperon. calreticulin. calcium binding protein of the endoplasmic reticulum.

AAD32207.1 AF134733 Prunus armeniaca
calcium-binding protein calreticulin.

CAA61939.1 X89813 Zea mays
Calreticulin precursor.

AAA32948.1 L27348 Hordeum vulgare
calcium binding protein. calreticulin. CRH1.

AAA32949.1 L27349 Hordeum vulgare
calcium binding protein. calreticulin. CRH2.

AAF01470.1 AF190454 Zea mays
calreticulin. CRT. calcium binding protein.

CAB54526.1 AJ000765 Chlamydomonas reinhardtii
calreticulin.

AAB70919.1 AF019376 *Brassica napus*
calreticulin. Crt1. calcium binding protein; similar to *A. thaliana* calreticulin encoded by
GenBank Accession Number U66343.

BAA85118.1 AB018243 *Solanum melongena*
calreticulin-like protein. EEF22.

CAA54975.1 X78057 *Zea mays*
calreticulin. CRH.

CAA57914.1 X82578 *Parthenium argentatum*
calreticulin. 111R.

AAK15502.1 AF325720 *Pennisetum ciliare*
calreticulin-like protein. Pcp4.

BAA77025.1 AB026251 *Lithospermum erythrorhizon*
calreticulin.

SEQ ID NO: 596

BAA12206.1 DS4061 *Spinacia oleracea*
phosphoserine aminotransferase.

SEQ ID NO: 597

AAF73124.1 AF148534 *Lycopersicon esculentum*
whitefly-induced gp91-phox. Wf1. mammalian gp91-phox homolog; respiratory burst
oxidase homolog; putative NADPH oxidase; similar to neutrophil NADPH oxidase gp91-
phox subunit; similar to *Arabidopsis thaliana* Rboh and *Oryza sativa* Rboh; similar to
Caenorhabditis elegans PhoX-like proteins.

AAF73104.1 AF147783 *Lycopersicon esculentum*
whitefly-induced gp91-phox. Wf1. mammalian gp91-phox homolog; respiratory burst
oxidase homolog; putative NADPH oxidase; similar to neutrophil NADPH oxidase gp1-phox
subunit; similar to *Arabidopsis thaliana* Rboh and *Oryza sativa* Rboh.

AAD25300.1 AF088276 *Lycopersicon esculentum*
NADPH oxidase. RBOH1. gp91; phox homolog.

AAB87790.1 AF015302 *Oryza sativa*
RbohAOsp. putative NADPH oxidase; intrinsic plasma membrane protein; similar to the
neutrophil NADPH oxidase gp91phox subunit; contains RanGAP1 domain; similar to *O.*
sativa NAD(P)H oxidase sequence with GenBank Accession Number X93301.

CAA63704.1 X93301 *Oryza sativa*
NAD(P)H oxidase. rbohA.

AAD24966.1 AF109150 *Lycopersicon esculentum*
NADPH oxidase. gp91; phox homolog.

AAD25225.1 AF088279 *Potamogeton crispus*
NADPH oxidase. RBOH1. gp91; phox homolog.

SEQ ID NO: 599

CAC21424.1 AJ278332 *Lycopersicon esculentum*
involved in octadecanoid biosynthesis. 12-oxophytodienoate reductase 3. opr3.

BAB40340.1 AB044940 *Pisum sativum*
12-oxophytodienoic acid 10, 11-reductase. OPDAR.

CAB43506.1	AJ242551	<i>Lycopersicon esculentum</i> involved in jasmonic acid biosynthesis. 12-oxophytodienoate reductase. opr.
CAC21423.1	AJ278331	<i>Lycopersicon esculentum</i> involved in octadecanoid biosynthesis. putative 12-oxophytodienoate reductase 2. opr2.
CAB97122.1	AJ297421	<i>Daucus carota</i> oxidoreductase. putative 12-oxophytodienoate reductase. opr2.
SEQ ID NO: 602		
AAB37246.1	U58971	<i>Nicotiana tabacum</i> calmodulin-binding protein. TCB60.
SEQ ID NO: 603		
AAK15006.1	AF233433	<i>Brassica napus</i> arginase. similar to <i>Arabidopsis thaliana</i> and <i>Glycine max</i> arginase.
AAK07744.1	AF130440	<i>Pinus taeda</i> converts L-arginine to L-ornithine and urea. arginase. ARS20. L-arginine amidinohydrolase.
AAC04613.1	AF035671	<i>Glycine max</i> hydrolysis of L-Arg to L-Orn and urea. arginase. pAG1. L-Arg amidinohydrolase.
SEQ ID NO: 605		
CAA81210.1	Z26251	<i>Helianthus tuberosus</i> Catalyzes the reduction of cytochrome P450 in microsomes. NADPH-ferrihemoprotein reductase.
AAB02721.1	U58629	<i>Helianthus tuberosus</i> NADPH-ferrihemoprotein oxidoreductase. HTR2. NADPH-cytochrome P450 reductase isoform.
CAC27143.1	AJ132538	<i>Picea abies</i> NADPH-cytochrome P450 reductase.
AAA79131.1	U10545	<i>Chlamydomonas reinhardtii</i> ferredoxin-NADP+ reductase. fnr.
CAA55406.1	X78851	<i>Chlamydomonas reinhardtii</i> ferredoxin NADP reductase.
AAB40978.1	U22328	<i>Volvox carteri</i> ferredoxin-NADP+ reductase. fnr. FNR.
AAA33029.1	M25528	<i>Mesembryanthemum crystallinum</i> ferredoxin-NADP+ reductase precursor (fnrA; EC 1.6.7.1).
CAA30978.1	X12446	<i>Pisum sativum</i> ferredoxin-NADH+ reductase preprotein (AA -52 to 308).
BAA13417.1	D87547	<i>Oryza sativa</i> precursor ferredoxin-NADP+ oxidoreductase.
AAA21758.1	U14956	<i>Vicia faba</i> photosynthetic electron transport. ferredoxin NADP+ reductase precursor. fnr.
AAA34029.1	M86349	<i>Spinacia oleracea</i> ferredoxin-NADP oxidoreductase. precursor protein.
CAB71293.1	AJ250378	<i>Capsicum annuum</i> chloroplast ferredoxin-NADP+ oxidoreductase precursor. fnr.

CAA74359.1	Y14032	Nicotiana tabacum	ferredoxin--NADP(+) reductase. fnr.
BAA88236.1	AB035644	Zea mays	NADP+ oxidoreductase. ferredoxin. L-FNRI.
BAA88237.1	AB035645	Zea mays	NADP+ oxidoreductase. ferredoxin. L-FNRII.
BAA20365.1	AB004307	Nicotiana tabacum	ferredoxin-NADP oxidoreductase.
BAA07479.1	D38445	Oryza sativa	root ferredoxin-NADP+ reductase. root FNR. nitrate assimilation pathway.
BAA02248.1	D12815	Oryza sativa	ferredoxin-NADP+ reductase enzyme.
BAA04232.1	D17410	Oryza sativa	ferredoxin-NADP+ reductase.
BAA90642.1	AP001129	Oryza sativa	ESTs AU078647(E1557),C72400(E1557) correspond to a region of the predicted gene.; Similar to Oryza sativa, ferredoxin-NADP+ reductase. (D17790).
BAA85425.1	AP000616	Oryza sativa	ESTs AU078647(E1557),C72400(E1557) correspond to a region of the predicted gene.; similar to ferredoxin-NADP+ reductase (D17790).
BAA04616.1	D17790	Oryza sativa	ferredoxin-NADP+ reductase.
AAB40034.1	U10418	Zea mays	ferredoxin-NADP reductase precursor.
CAA67796.1	X99419	Pisum sativum	ferredoxin NADP oxidoreductase.
AAK09367.1	AF321525	Pisum sativum	ferredoxin-NADP+ reductase. FNR.
AAK09370.1	AF321528	Pisum sativum	ferredoxin-NADP+ reductase. FNR.
AAK09369.1	AF321527	Pisum sativum	ferredoxin-NADP+ reductase. FNR.
AAK09368.1	AF321526	Pisum sativum	ferredoxin-NADP+ reductase. FNR.
SEQ ID NO: 606			
BAA82107.1	AB022693	Nicotiana tabacum	transcription factor. NtWRKY1.
AAC31956.1	AF080595	Pimpinella brachycarpa	zinc finger protein. ZFP1. WRKY1.
AAC49527.1	U48831	Petroselinum crispum	WRKY1. contains two WRKY domains; WRKY-type DNA-binding protein; sequence-specific DNA-binding protein.

AAD55974.1	AF121353	Petroselinum crispum	zinc-finger type transcription factor WRKY1. WRKY1.
BAA77383.1	AB020590	Nicotiana tabacum	transcription factor NtWRKY2.
AAD32677.1	AF140554	Avena sativa	DNA-binding protein WRKY1. wrky1. putative transcription factor.
CAA88326.1	Z48429	Avena fatua	binds conserved cis-element from cereal alpha-Amy2 promoters. DNA-binding protein.
BAA86031.1	AB026890	Nicotiana tabacum	transcription factor NtWRKY4.
AAD16139.1	AF096299	Nicotiana tabacum	DNA-binding protein 2. WRKY2. transcription factor.
AAC37515.1	L44134	Cucumis sativus	SPF1-like DNA-binding protein.
AAF23898.1	AF193802	Oryza sativa	zinc finger transcription factor WRKY1.
AAK16171.1	AC079887	Oryza sativa	putative DNA-binding protein. OSJNBa0040E01.10.
AAC49529.1	U58540	Petroselinum crispum	WRKY2. Contains two WRKY domains; WRKY-type DNA-binding protein.
AAD16138.1	AF096298	Nicotiana tabacum	DNA-binding protein 1. WRKY1. transcription factor.
BAB19096.1	AP002839	Oryza sativa	putative DNA-binding protein homolog. P0688A04.2.
BAB19075.1	AP002744	Oryza sativa	putative DNA-binding protein homolog. P0006C01.17.
AAK16170.1	AC079887	Oryza sativa	putative DNA binding protein. OSJNBa0040E01.4.
CAB97004.1	AJ278507	Solanum tuberosum	putative transcription factor. WRKY DNA binding protein. WRKY1.
BAB18313.1	AP002865	Oryza sativa	putative WRKY DNA binding protein. P0034C11.1. contains EST C26525(C12525).
AAD38283.1	AC007789	Oryza sativa	putative WRKY DNA binding protein. OSJNBa0049B20.9.
BAB40073.1	AP003074	Oryza sativa	putative WRKY DNA binding protein. OSJNBa0004G10.20. contains EST C26525(C12525).
AAC49528.1	U56834	Petroselinum crispum	DNA-binding. WRKY3. WRKY-type DNA-binding protein.
BAB16432.1	AB041520	Nicotiana tabacum	WRKY transcription factor Nt-SubD48. Nt-SubD48.
BAA77358.1	AB020023	Nicotiana tabacum	WRKY domain Zn-finger type DNA-binding protein. DNA-binding protein NtWRKY3.

AAD32676.1	AF140553	Avena sativa	DNA-binding protein WRKY3. wrky3. putative transcription factor.
CAA88331.1	Z48431	Avena fatua	binds conserved cis-element from cereal alpha-Amy2 promoters. DNA-binding protein.
AAG35658.1	AF204925	Petroselinum crispum	transcription factor WRKY4. WRKY4. binds to W box (TTGACC) elements.
AAG46150.1	AC018727	Oryza sativa	putative DNA-binding protein. OSJNBa0056G17.18.
AAD27591.1	AF121354	Petroselinum crispum	binds sequence specifically to W Boxes (TTGACC). transcription factor. WRKY3. sequence specific DNA-binding protein.
AAG35659.1	AF204926	Petroselinum crispum	transcription factor WRKY5. WRKY5. binds to W box (TTGACC) elements.
CAB66338.1	AJ279697	Betula pendula	wrky-type DNA binding protein. wrky.
AAF61864.1	AF193771	Nicotiana tabacum	DNA-binding protein 4. WRKY4. transcription factor.
AAF61863.1	AF193770	Nicotiana tabacum	DNA-binding protein 3. WRKY3. transcription factor.
SEQ ID NO: 608			
BAAS7853.1	AP000816	Oryza sativa	EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
AAK21965.1	AY028699	Brassica napus	receptor protein kinase PERK1.
BAB21240.1	AP002953	Oryza sativa	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
BAB19337.1	AP003044	Oryza sativa	putative protein kinase. P0038C05.10. contains ESTs AU056335(S20481),AU056336(S20481).
BAA92836.1	AB032473	Brassica oleracea	S18 S-locus receptor kinase. SRK18.
AAB61708.1	U93048	Daucus carota	somatic embryogenesis receptor-like kinase. SERK.
BAA23676.1	AB000970	Brassica rapa	receptor kinase 1. BcRK1.
AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.
BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
AAD21872.1	AF078082	Phaseolus vulgaris	receptor-like protein kinase homolog RK20-1.

CAB41878.1	Y18259	Brassica oleracea	SRK5 protein. SRK5. receptor-like kinase.
AAA62232.1	U00443	Brassica napus	S-receptor kinase. protein contains an immunoglobulin-like domain.
AAA33000.1	M76647	Brassica oleracea	receptor protein kinase. SKR6.
AAG59657.1	AC084319	Oryza sativa	putative protein kinase. OSJNBa0004B24.20.
CAB41879.1	Y18260	Brassica oleracea	SRK15 protein. SRK15. receptor-like kinase.
CAA73134.1	Y12531	Brassica oleracea	serine/threonine kinase. BRLK.
BAB16871.1	AP002537	Oryza sativa	putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
BAB18292.1	AP002860	Oryza sativa	putative receptor-like protein kinase. P0409B08.19.
BAA06285.1	D30049	Brassica rapa	S-receptor kinase SRK9.
BAA21132.1	D88193	Brassica rapa	S-receptor kinase. SRK9 (B.c).
CAB89179.1	AJ245479	Brassica napus subsp. napus	ser /thr kinase. S-locus receptor kinase. srk.
AAA33008.1	M97667	Brassica napus	serine/threonine kinase receptor.
CAA67145.1	X98520	Brassica oleracea	receptor-like kinase. SFR2.
CAA73133.1	Y12530	Brassica oleracea	serine /threonine kinase. ARLK.
AAF66615.1	AF142596	Nicotiana tabacum	LRR receptor-like protein kinase.
AAF76314.1	AF220603	Lycopersicon esculentum	Fen kinase. Lescfen.
AAK11568.1	AF318492	Lycopersicon hirsutum	Pto-like protein kinase B. LhirPtoB.
CAA74662.1	Y14286	Brassica oleracea	SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
AAB47424.1	U59317	Lycopersicon pimpinellifolium	serine/threonine protein kinase Fen. Fen. fenthion sensitivity gene from tomato.
AAB47422.1	U59318	Lycopersicon esculentum	serine/threonine protein kinase Fen. fen. allele of Fen, fenthion sensitivity gene from tomato.

AAC48932.1 U13923 *Lycopersicon pimpinellifolium*
Fen. putative serine/threonine protein kinase; similar to product encoded by *Lycopersicon pimpinellifolium* Pto gene, GenBank Accession Number U02271; Fen is a member of the Pto gene family.

AAF76307.1 AF220602 *Lycopersicon pimpinellifolium*
Fen kinase.

BAA07576.1 D38563 *Brassica rapa*
receptor protein kinase SRK8.

AAG16628.1 AY007545 *Brassica napus*
protein serine/threonine kinase BNK1.

CAA97692.1 Z73295 *Catharanthus roseus*
receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.

CAA79355.1 Z18921 *Brassica oleracea*
S-receptor kinase-like protein.

AAB93834.1 U82481 *Zea mays*
KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.

BAA92837.1 AB032474 *Brassica oleracea*
S60 S-locus receptor kinase. SRK60.

AAA33915.1 L27821 *Oryza sativa*
receptor type serine/threonine kinase. protein kinase.

SEQ ID NO: 610

BAB17348.1 AP002747 *Oryza sativa*
putative receptor kinase. P0698G03.32.

BAB17345.1 AP002747 *Oryza sativa*
putative receptor kinase. P0698G03.29.

BAB17126.1 AP002867 *Oryza sativa*
putative receptor kinase. P0463F06.16.

BAB39451.1 AP003338 *Oryza sativa*
putative receptor kinase. OJ1212_B09.24.

BAB17342.1 AP002747 *Oryza sativa*
putative receptor kinase. P0698G03.26.

AAC27489.1 AF077130 *Oryza sativa*
receptor-like protein kinase.

AAF78018.1 AF238474 *Oryza sativa*
receptor-like kinase. RLG16. protein kinase.

AAC02535.1 AF044260 *Oryza sativa*
receptor serine/threonine kinase. protein kinase.

BAB39435.1 AP003338 *Oryza sativa*
putative receptor kinase. OJ1212_B09.2.

AAD46917.1 AF164021 *Oryza sativa*
receptor kinase.

BAB39438.1	AP003338	Oryza sativa	putative receptor kinase. OJ1212_B09.7.
BAB17339.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.23.
AAC49629.1	U51330	Triticum aestivum	rust resistance kinase Lr10. LRK10.
BAB17321.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.1.
BAB17129.1	AP002867	Oryza sativa	putative receptor kinase. P0463F06.20.
AAF68398.1	AF237568	Oryza sativa	receptor-like protein kinase. RLG2.
BAB17331.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.12.
BAB17139.1	AP002867	Oryza sativa	putative receptor kinase. P0463F06.31.
AAC01746.1	AF044489	Oryza sativa	receptor-like protein kinase. drpk1.
AAF78016.1	AF238472	Oryza sativa	receptor-like kinase. RLG15. protein kinase.
BAB39441.1	AP003338	Oryza sativa	putative receptor kinase. OJ1212_B09.11.
BAB17116.1	AP002867	Oryza sativa	putative receptor kinase. P0463F06.3.
AAF78044.1	AF248493	Oryza sativa	receptor-like kinase. RLG18. protein kinase.
AAD44029.1	AF085164	Hordeum vulgare	receptor-like kinase LRK10.
BAB17332.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.13. contains ESTs D47575(S13157),AU032665(S13157).
BAB17347.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.31. contains ESTs D47575(S13157),AU032665(S13157).
BAB17344.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.28. contains ESTs D47575(S13157),AU032665(S13157).
BAB17337.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.21. contains ESTs D47575(S13157),AU032665(S13157).
BAB17335.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.17. contains ESTs D47575(S13157),AU032665(S13157).
BAB17115.1	AP002867	Oryza sativa	putative receptor kinase. P0463F06.2.
BAB39440.1	AP003338	Oryza sativa	putative receptor kinase. OJ1212_B09.10.

BAB39437.1	AP003338	Oryza sativa	receptor-like kinase. OJ1212_B09.6.
AAF78019.1	AF238475	Oryza sativa	receptor-like kinase. RLG17. protein kinase.
BAB17127.1	AP002867	Oryza sativa	putative receptor kinase. P0463F06.17.
AAD46916.1	AF164020	Oryza sativa	receptor kinase.
AAF78021.1	AF238477	Oryza sativa	receptor-like kinase. RLG5. protein kinase.
AAD46417.1	AF100767	Oryza sativa	receptor-like kinase. 8ARK3. similar to wheat ARK1AS.
AAD46415.1	AF100765	Oryza sativa	receptor-like kinase. 8ARK1. similar to wheat ARK1AS.
BAB17128.1	AP002867	Oryza sativa	putative receptor kinase. P0463F06.18.
AAF68400.1	AF237570	Oryza sativa	receptor-like protein kinase. RLG3.
BAB17323.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.3.
BAB17131.1	AP002867	Oryza sativa	putative receptor kinase. P0463F06.22.
AAF68397.1	AF237567	Oryza sativa	receptor-like protein kinase. RLG1.
AAF78015.1	AF238471	Oryza sativa	receptor-like kinase. RLG10. protein kinase.
AAD43962.1	U78762	Triticum aestivum	receptor-like kinase ARK1AS. ARK1AS.
SEQ ID NO: 611			
BAA78764.1	AB023482	Oryza sativa	ESTs C98382(C2985),D22444(C11129) correspond to a region of the predicted gene.; Similar to Arabidopsis thaliana APK1 gene for protein tyrosine-serine-threonine kinase.(D12522).
AAK11674.1	AF339747	Lophopyrum elongatum	protein kinase. ESI47.
AAF43496.1	AF131222	Lophopyrum elongatum	protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.
AAG16628.1	AY007545	Brassica napus	protein serine/threonine kinase BNK1.
BAA94509.1	AB041503	Populus nigra	protein kinase 1. PnPK1.
BAA94510.1	AB041504	Populus nigra	protein kinase 2. PnPK2.

BAB07999.1	AP002525	Oryza sativa	putative protein kinase. P0462H08.22. contains EST C22619(S11214).
BAB03429.1	AP002817	Oryza sativa	EST C22619(S11214) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).
BAA87853.1	AP000816	Oryza sativa	EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
BAB16871.1	AP002537	Oryza sativa	putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
BAB39409.1	AP002901	Oryza sativa	putative protein kinase. P0456F08.9. contains EST C23560(R0290).
CAB51834.1	00069	Oryza sativa	11332.5. contains eukaryotic protein kinase domain PF.
BAB21240.1	AP002953	Oryza sativa	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.
BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
AAK11567.1	AF318491	Lycopersicon hirsutum	Pto-like protein kinase F. LhirPtoF.
BAA90808.1	AP001168	Oryza sativa	Similar to putative receptor-like protein kinase (AL035679).
AAK21965.1	AY028699	Brassica napus	receptor protein kinase PERK1.
AAC48932.1	U13923	Lycopersicon pimpinellifolium	Fen. putative serine/threonine protein kinase; similar to product encoded by Lycopersicon pimpinellifolium Pto gene, GenBank Accession Number U02271; Fen is a member of the Pto gene family.
AAB47424.1	U59317	Lycopersicon pimpinellifolium	serine/threonine protein kinase Fen. Fen. fenthion sensitivity gene from tomato.
AAF76307.1	AF220602	Lycopersicon pimpinellifolium	Fen kinase.
AAK11566.1	AF318490	Lycopersicon hirsutum	Pto-like protein kinase E. LhirPtoE. confers resistance to bacterial speck disease.
AAG03090.1	AC073405	Oryza sativa	Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).
AAF76314.1	AF220603	Lycopersicon esculentum	Fen kinase. Lescfen.

AAB47421.1	U59316	<i>Lycopersicon esculentum</i> serine/threonine protein kinase Pto. pto. allele of Pto bacterial speck disease resistance gene in tomato.
AAF76313.1	AF220603	<i>Lycopersicon esculentum</i> Pto kinase. LescPth5.
AAB47422.1	U59318	<i>Lycopersicon esculentum</i> serine/threonine protein kinase Fen. fen. allele of Fen, fenthion sensitivity gene from tomato.
AAG59657.1	AC084319	<i>Oryza sativa</i> putative protein kinase. OSJNBa0004B24.20.
AAF76306.1	AF220602	<i>Lycopersicon pimpinellifolium</i> Pto kinase.
AAB47423.1	U59315	<i>Lycopersicon pimpinellifolium</i> serine/threonine protein kinase Pto. Pto. bacterial speck disease resistance in tomato; disease resistance gene.
AAC48914.1	U02271	<i>Lycopersicon pimpinellifolium</i> protein kinase.
AAK11568.1	AF318492	<i>Lycopersicon hirsutum</i> Pto-like protein kinase B. LhirPtoB.
BAB21241.1	AP002953	<i>Oryza sativa</i> Putative Pto kinase interactor 1. P0426D06.21. contains ESTs AU108280(E0721),D48017(S13927).
AAC27894.1	AF023164	<i>Zea mays</i> leucine-rich repeat transmembrane protein kinase 1. ltk1.
AAF91337.1	AF249318	<i>Glycine max</i> Ptil kinase-like protein. Ptilb. protein kinase.
AAC61805.1	U28007	<i>Lycopersicon esculentum</i> serine/threonine protein kinase. Pto kinase interactor 1. Ptil. Ptil kinase.
CAA97692.1	Z73295	<i>Catharanthus roseus</i> receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
AAF91336.1	AF249317	<i>Glycine max</i> Ptil kinase-like protein. Ptila. protein kinase.
AAF66615.1	AF142596	<i>Nicotiana tabacum</i> LRR receptor-like protein kinase.
AAB61708.1	U93048	<i>Daucus carota</i> somatic embryogenesis receptor-like kinase. SERK.
AAK11569.1	AF318493	<i>Lycopersicon hirsutum</i> Pto-like protein kinase D. LhirPtoD.
BAA92221.1	AP001278	<i>Oryza sativa</i> Similar to <i>Arabidopsis thaliana</i> chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).
BAA87852.1	AP000816	<i>Oryza sativa</i> Similar to putative Ser/Thr protein kinase. (AC004218).

AAC27895.1 AF023165 Zea mays
leucine-rich repeat transmembrane protein kinase 2. ltk2.

SEQ ID NO: 612

CAA54613.1 X77463 Manihot esculenta
UTP-glucose glucosyltransferase. CGT6.

CAA54609.1 X77459 Manihot esculenta
UTP-glucose glucosyltransferase. CGT1.

CAA54611.1 X77461 Manihot esculenta
UTP-glucose glucosyltransferase. CGT2.

CAA54612.1 X77462 Manihot esculenta
UTP-glucose glucosyltransferase. CGT5.

BAB17182.1 AP002843 Oryza sativa
putative UTP-glucose glucosyltransferase. P0407B12.19.

BAB17176.1 AP002843 Oryza sativa
putative UTP-glucose glucosyltransferase. P0407B12.13.

CAB56231.1 Y18871 Dorotheanthus bellidiformis
betanidin-5-O-glucosyltransferase.

BAA83484.1 AB031274 Scutellaria baicalensis
UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.

AAB36653.1 U32644 Nicotiana tabacum
immediate-early salicylate-induced glucosyltransferase. IS5a.

AAK28303.1 AF346431 Nicotiana tabacum
phenylpropanoid:glucosyltransferase 1. togt1. glucosyltransferase.

CAA59450.1 X85138 Lycopersicon esculentum
twil. homologous to glucosyltransferases.

AAB36652.1 U32643 Nicotiana tabacum
immediate-early salicylate-induced glucosyltransferase. IS10a.

AAK28304.1 AF346432 Nicotiana tabacum
phenylpropanoid:glucosyltransferase 2. togt2. glucosyltransferase.

BAA89009.1 AB027455 Petunia x hybrida
anthocyanin 5-O-glucosyltransferase. PH1.

AAG25643.1 AF303396 Phaseolus vulgaris
UDP-glucosyltransferase HRA25. putative; defense associated.

AAF61647.1 AF190634 Nicotiana tabacum
UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.

BAA93039.1 AB033758 Citrus unshiu
limonoid UDP-glucosyltransferase. LGTase.

AAB48444.1 U82367 Solanum tuberosum
UDP-glucose glucosyltransferase.

AAD21086.1 AF127218 Forsythia x intermedia
adds glucose residue to position 3 of flavonoid compounds. flavonoid 3-O-
glucosyltransferase. UFGT.

AAK16175.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.15.
CAC09351.1	AL442007	Oryza sativa	putative glucosyltransferase. H0212B02.7.
AAD04166.1	AF101972	Phaseolus lunatus	catalyzes formation of O-glucosylzeatin from zeatin and UDPG; catalyzes formation of O-xylosylzeatin from zeatin and UDPX. zeatin O-glucosyltransferase. ZOG1. cytokinin O-glucosyltransferase.
AAF17077.1	AF199453	Sorghum bicolor	UDP-glucose glucosyltransferase. UDP-glucose:p-hydroxymandelonitrile-o-glucosyltransferase.
BAA12737.1	D85186	Gentiana triflora	UDP-glucose:flavonoid-3-glucosyltransferase.
BAB07962.1	AP002524	Oryza sativa	putative anthocyanin 5-O-glucosyltransferase. P0406H10.16. contains ESTs AU067881(C10481),AU067882(C10481).
BAA36421.1	AB013596	Perilla frutescens	UDP-glucose:anthocyanin 5-O-glucosyltransferase. PF3R4.
CAA54610.1	X77460	Manihot esculenta	UTP-glucose glucosyltransferase. CGT4.
AAF98390.1	AF287143	Brassica napus	catalyzes the transfer of glucose from UDP-glucose to sinapate and some other hydroxycinnamates (4-coumarate, caffeate, ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.
BAA36423.1	AB013598	Verbena x hybrida	UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.
CAA30760.1	X07937	Zea mays	UDPglucose flavonoid glycosyl transferase. Bz-W22.
CAA30761.1	X07940	Zea mays	UDPglucose flavonoid glycosyl-transferase. Bz-McC.
CAA31855.1	X13500	Zea mays	UDPglucose:flavonol 3-O-glucosyltransferase.
BAA19659.1	AB002818	Perilla frutescens	flavonoid 3-O-glucosyltransferase. UDP glucose.
BAA89008.1	AB027454	Petunia x hybrida	anthocyanidin 3-O-glucosyltransferase. PGT8.
AAK16172.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.14.
SEQ ID NO: 613			
CAA54609.1	X77459	Manihot esculenta	UTP-glucose glucosyltransferase. CGT1.
CAA54613.1	X77463	Manihot esculenta	UTP-glucose glucosyltransferase. CGT6.

CAA54611.1	X77461	Manihot esculenta	UTP-glucose glucosyltransferase. CGT2.
CAA54612.1	X77462	Manihot esculenta	UTP-glucose glucosyltransferase. CGT5.
BAB17182.1	AP002843	Oryza sativa	putative UTP-glucose glucosyltransferase. P0407B12.19.
BAB17176.1	AP002843	Oryza sativa	putative UTP-glucose glucosyltransferase. P0407B12.13.
CAB56231.1	Y18871	Dorotheanthus bellidiformis	betanidin-5-O-glucosyltransferase.
AAB36653.1	U32644	Nicotiana tabacum	immediate-early salicylate-induced glucosyltransferase. IS5a.
AAK28303.1	AF346431	Nicotiana tabacum	phenylpropanoid:glucosyltransferase 1. togt1. glucosyltransferase.
AAB36652.1	U32643	Nicotiana tabacum	immediate-early salicylate-induced glucosyltransferase. IS10a.
AAK28304.1	AF346432	Nicotiana tabacum	phenylpropanoid:glucosyltransferase 2. togt2. glucosyltransferase.
CAA59450.1	X85138	Lycopersicon esculentum	twil. homologous to glucosyltransferases.
BAA83484.1	AB031274	Scutellaria baicalensis	UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.
AAF61647.1	AF190634	Nicotiana tabacum	UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.
BAA93039.1	AB033758	Citrus unshiu	limonoid UDP-glucosyltransferase. LGTase.
AAB48444.1	U82367	Solanum tuberosum	UDP-glucose glucosyltransferase.
BAA89009.1	AB027455	Petunia x hybrida	anthocyanin 5-O-glucosyltransferase. PH1.
BAA36421.1	AB013596	Perilla frutescens	UDP-glucose:anthocynin 5-O-glucosyltransferase. PF3R4.
CAC09351.1	AL442007	Oryza sativa	putative glucosyltransferase. H0212B02.7.
BAA12737.1	D85186	Gentiana triflora	UDP-glucose:flavonoid-3-glucosyltransferase.
AAG25643.1	AF303396	Phaseolus vulgaris	UDP-glucosyltransferase HRA25. putative; defense associated.
AAD04166.1	AF101972	Phaseolus lunatus	catalyzes formation of O-glucosylzeatin from zeatin and UDPG; catalyzes formation of O-xylosylzeatin from zeatin and UDPX. zeatin O-glucosyltransferase. ZOG1. cytokinin O-glucosyltransferase.

CAA54610.1	X77460	Manihot esculenta	UTP-glucose glucosyltransferase. CGT4.
AAF98390.1	AF287143	Brassica napus	catalyzes the transfer of glucose from UDP-glucose to sinapate and some other hydroxycinnamates (4-coumarate, caffeate, ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.
AAK16172.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.14.
BAA36423.1	AB013598	Verbena x hybrida	UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.
AAD21086.1	AF127218	Forsythia x intermedia	adds glucose residue to position 3 of flavonoid compounds. flavonoid 3-O-glucosyltransferase. UFGT.
AAF17077.1	AF199453	Sorghum bicolor	UDP-glucose glucosyltransferase. UDP-glucose:p-hydroxymandelonitrile-o-glucosyltransferase.
AAK16175.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.15.
BAB07962.1	AP002524	Oryza sativa	putative anthocyanin 5-O-glucosyltransferase. P0406H10.16. contains ESTs AU067881(C10481),AU067882(C10481).
CAA31855.1	X13500	Zea mays	UDPglucose:flavonol 3-O-glucosyltransferase.
BAA36422.1	AB013597	Perilla frutescens	UDP-glucose:anthocyanin 5-O-glucosyltransferase homologue. PF3R6.
BAA89008.1	AB027454	Petunia x hybrida	anthocyanidin 3-O-glucosyltransferase. PGT8.
SEQ ID NO: 614			
AAD21872.1	AF078082	Phaseolus vulgaris	receptor-like protein kinase homolog RK20-1.
CAA73134.1	Y12531	Brassica oleracea	serine/threonine kinase. BRLK.
AAB93834.1	U82481	Zea mays	KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
AAA33008.1	M97667	Brassica napus	serine/threonine kinase receptor.
CAB89179.1	AJ245479	Brassica napus subsp. napus	ser /thr kinase. S-locus receptor kinase. srk.
AAA33000.1	M76647	Brassica oleracea	receptor protein kinase. SKR6.
BAA23676.1	AB000970	Brassica rapa	receptor kinase 1. BcRK1.

BAA06285.1	D30049	Brassica rapa	S-receptor kinase SRK9.
BAA21132.1	D88193	Brassica rapa	S-receptor kinase. SRK9 (B.c).
CAA74661.1	Y14285	Brassica oleracea	SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.
BAA92837.1	AB032474	Brassica oleracea	S60 S-locus receptor kinase. SRK60.
BAA07577.2	D38564	Brassica rapa	receptor protein kinase SRK12.
BAA07576.1	D38563	Brassica rapa	receptor protein kinase SRK8.
CAA73133.1	Y12530	Brassica oleracea	serine /threonine kinase. ARLK.
AAC23542.1	U20948	Ipomoea trifida	receptor protein kinase. IRK1.
CAA79355.1	Z18921	Brassica oleracea	S-receptor kinase-like protein.
CAA67145.1	X98520	Brassica oleracea	receptor-like kinase. SFR2.
CAA74662.1	Y14286	Brassica oleracea	SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
BAB21001.1	AB054061	Brassica rapa	S locus receptor kinase. SRK22.
AAA62232.1	U00443	Brassica napus	S-receptor kinase. protein contains an immunoglobulin-like domain.
CAB41879.1	Y18260	Brassica oleracea	SRK15 protein. SRK15. receptor-like kinase.
CAB41878.1	Y18259	Brassica oleracea	SRK5 protein. SRK5. receptor-like kinase.
BAA92836.1	AB032473	Brassica oleracea	S18 S-locus receptor kinase. SRK18.
BAB18292.1	AP002860	Oryza sativa	putative receptor-like protein kinase. P0409B08.19.
AAD52097.1	AF088885	Nicotiana tabacum	receptor-like kinase CHRK1. Chrk1.
AAA33915.1	L27821	Oryza sativa	receptor type serine/threonine kinase. protein kinase.
BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).

BAB16871.1	AP002537	Oryza sativa	putative protein kinase APK1A Arabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192), D25110(R3192).
AAK21965.1	AY028699	Brassica napus	receptor protein kinase PERK1.
AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.
BAA94529.2	AP001800	Oryza sativa	Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAA94509.1	AB041503	Populus nigra	protein kinase 1. PnPK1.
BAA94510.1	AB041504	Populus nigra	protein kinase 2. PnPK2.
BAA87853.1	AP000816	Oryza sativa	EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
BAB39409.1	AP002901	Oryza sativa	putative protein kinase. P0456F08.9. contains EST C23560(R0290).
AAG03090.1	AC073405	Oryza sativa	Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).
BAA92954.1	AP001551	Oryza sativa	Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).
BAA94518.1	AP001800	Oryza sativa	Similar to Arabidopsis thaliana chromosome 2 section 111 of 255; putative receptor-like protein kinase (AC002392).
BAB07904.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.12.
SEQ ID NO: 619			
CAA72092.1	Y11209	Nicotiana tabacum	protein disulfide-isomerase precursor. PDI.
AAG13988.1	AF298829	Prunus avium	putative protein disulfide-isomerase. PDI.
AAD02069.1	AF036939	Chlamydomonas reinhardtii	redox-regulator of 5'UTR psbA mRNA binding complex and translation. protein disulfide isomerase. localized to ER and chloroplast.
AAC49896.1	AF027727	Chlamydomonas reinhardtii	involved in the redox-regulated binding of chloroplast poly(A)-binding protein to the 5'-UTR of psbA mRNA; regulates chloroplast translational activation. protein disulfide isomerase RB60. PDI.
AAD55566.1	AF110784	Volvox carteri f. nagariensis	protein disulfide isomerase precursor. pdi.
AAB08519.1	L39014	Zea mays	protein disulfide isomerase. pdi. putative.

AAA70344.1 L33250 *Hordeum vulgare*
catalyze the formation of disulfide bonds. disulfide isomerase. PDI. putative.

AAA70345.1 L33251 *Hordeum vulgare*
catalyze the formation of disulfide bonds. disulfide isomerase. PDI. putative.

CAC21230.1 AJ277379 *Triticum turgidum* subsp. durum
catalyzes formation of disulfide bonds. protein disulfide isomerase. Pdi.

AAA19660.1 U11496 *Triticum aestivum*
protein disulfide isomerase. PDI.

CAC21231.1 AJ277380 *Triticum turgidum* subsp. durum
catalyzes formation of disulfide bonds. protein disulfide isomerase. Pdi.

CAC21229.1 AJ277378 *Triticum turgidum* subsp. durum
catalyzes formation of disulfide bonds. protein disulfide isomerase. Pdi.

CAC21228.1 AJ277377 *Triticum turgidum* subsp. durum
catalyzes the formation of disulfide bonds. protein disulfide isomerase. Pdi.

AAB05641.1 U41385 *Ricinus communis*
protein disulphide isomerase PDI. molecular chaperone.

CAA77575.1 Z11499 *Medicago sativa*
protein disulfide isomerase.

AAD28260.1 AF131223 *Datisca glomerata*
protein disulfide isomerase homolog. PDI.

AAA70346.1 L33252 *Hordeum vulgare*
catalyze the formation of disulfide bonds. disulfide isomerase. PDI. putative.

BAA92322.1 AB039278 *Oryza sativa*
protein disulfide isomerase. Pdi.

BAA77026.1 AB026252 *Lithospermum erythrorhizon*
disulfide-isomerase precursor.

AAC79709.1 AF093614 *Acetabularia acetabulum*
putative protein disulfide isomerase.

SEQ ID NO: 620

CAA64413.1 X94943 *Lycopersicon esculentum*
peroxidase. cevil6.

AAA32676.1 M37637 *Arachis hypogaea*
cationic peroxidase. PNC2.

BAA82307.1 AB027753 *Nicotiana tabacum*
peroxidase.

AAB67737.1 L77080 *Stylosanthes humilis*
cationic peroxidase.

AAD37429.2 AF149279 *Phaseolus vulgaris*
peroxidase 4 precursor. FBP4. secretory peroxidase.

CAA71494.1 Y10468 *Spinacia oleracea*
peroxidase. prxr7.

AAD37375.1	AF145349	Glycine max peroxidase. Prx3.
AAF63024.1	AF244921	Spinacia oleracea hydrogen peroxide catabolism. peroxidase prx12 precursor. type III peroxidase.
CAA66037.1	X97351	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
BAB39274.1	AP002971	Oryza sativa putative peroxidase. P0537A05.2.
AAA65637.1	L13654	Lycopersicon esculentum peroxidase. TPX1.
CAA40796.1	X57564	Armoracia rusticana peroxidase. peroxidase precursor.
AAD11482.1	U51192	Glycine max peroxidase precursor. sEPa2.
CAA80502.1	Z22920	Spirodela polyrrhiza peroxidase.
BAA77387.1	AB024437	Scutellaria baicalensis peroxidase 1.
CAA59485.1	X85228	Triticum aestivum peroxidase. POX2.
BAA07663.1	D42064	Nicotiana tabacum cationic peroxidase isozyme 38K precursor.
BAA11853.1	D83225	Populus nigra peroxidase.
BAA07664.1	D42065	Nicotiana tabacum cationic peroxidase isozyme 40K precursor.
AAD37430.1	AF149280	Phaseolus vulgaris peroxidase 5 precursor. FBP5. secretory peroxidase.
AAD11481.1	U51191	Glycine max peroxidase precursor. sEPa1.
CAB94692.1	AJ242742	Ipomoea batatas Removal of H ₂ O ₂ , oxidation of toxic reductants, defence response toward wounding. peroxidase. pod.
BAA03644.1	D14997	Oryza sativa peroxidase.
AAD43561.1	AF155124	Gossypium hirsutum bacterial-induced peroxidase precursor. Perx_Goshiko.
BAA06334.1	D30652	Populus kitakamiensis peroxidase.
BAA92500.1	AP001383	Oryza sativa ESTs D39300(R3292), AU030751(E60187) correspond to a region of the predicted gene. Similar to peroxidase ATP6a. (X98774).

BAA90365.1	AP001081	Oryza sativa	ESTs D24550(R2151),D24265(R1609),AU031848(R2151) correspond to a region of the predicted gene. Similar to cationic peroxidase isozyme 40K precursor (D42065).
BAA89584.1	AP001073	Oryza sativa	ESTs D24550(R2151),D24265(R1609),AU031848(R2151) correspond to a region of the predicted gene. Similar to cationic peroxidase isozyme 40K precursor (D42065).
AAF34416.1	AF172282	Oryza sativa	putative peroxidase. DUPR11.5.
AAC49820.1	AF014469	Oryza sativa	peroxidase. POX5.1. wound inducible.
CAA66034.1	X97348	Populus balsamifera subsp. trichocarpa	signal for ER. peroxidase.
BAB39281.1	AP002971	Oryza sativa	putative peroxidase. P0537A05.10. contains ESTs D24657(R2329),AU082066(R2329).
BAA14144.1	D90116	Armoracia rusticana	peroxidase isozyme.
AAB97734.1	AF014502	Glycine max	seed coat peroxidase precursor. Ep. H ₂ O ₂ oxidoreductase; class III plant peroxidase.
CAA37713.1	X53675	Triticum aestivum	peroxidase.
AAC05277.1	AF049881	Linum usitatissimum	peroxidase FLXPER4. PER4.
CAA66035.1	X97349	Populus balsamifera subsp. trichocarpa	signal for ER. peroxidase.
BAA06335.1	D30653	Populus kitakamiensis	peroxidase.
CAA39486.1	X56011	Triticum aestivum	peroxidase.
BAA03911.1	D16442	Oryza sativa	peroxidase.
BAA94962.1	AB042103	Asparagus officinalis	peroxidase. AspPOX1.
AAC49821.1	AF014470	Oryza sativa	peroxidase. POXgX9. expressed in roots.
AAD37427.1	AF149277	Phaseolus vulgaris	peroxidase 1 precursor. FBPl. secretory peroxidase.
CAA76374.2	Y16776	Spinacia oleracea	peroxidase. prx10.
BAA08499.1	D49551	Oryza sativa	peroxidase. poxN.
CAA66036.1	X97350	Populus balsamifera subsp. trichocarpa	signal for ER. peroxidase.

AAA34108.1	J02979	Nicotiana tabacum	lignin-forming peroxidase precursor (EC 1.11.1.7).
CAA62226.1	X90693	Medicago sativa	peroxidase1B. prx1B.
CAA59487.1	X85230	Triticum aestivum	peroxidase. pox4.
SEQ ID NO: 626			
CAA98160.1	Z73932	Lotus japonicus	GTP-binding protein. RAB1C. rab1C.
BAA76422.1	AB024994	Cicer arietinum	rab-type small GTP-binding protein.
BAA02116.1	D12548	Pisum sativum	GTP-binding protein.
CAA69701.1	Y08425	Nicotiana plumbaginifolia	small GTP-binding protein. Rab1 subfamily.
AAA80678.1	U38464	Lycopersicon esculentum	small GTP-binding protein. LeRab1A. ; YPT1/Rab1A homolog LeRab1A.
BAA02118.1	D12550	Pisum sativum	GTP-binding protein.
AAB97115.1	U58854	Glycine max	small GTP-binding protein. sra2.
CAA51011.1	X72212	Nicotiana tabacum	ras-related GTP-binding protein. ypt2 homologue.
AAF65510.1	AF108883	Capsicum annuum	small GTP-binding protein.
AAA80680.1	U38466	Lycopersicon esculentum	small GTP-binding protein. LeRab1C. ; YPT1/Rab1A homolog LeRab1C.
CAA98161.1	Z73933	Lotus japonicus	GTP-binding protein. RAB1D. rab1D.
BAA02117.1	D12549	Pisum sativum	GTP-binding protein.
CAA98162.1	Z73934	Lotus japonicus	GTP-binding protein. RAB1E. rab1E.
AAA50159.1	L27417	Glycine max	GTP binding protein.
AAB28535.1	S66160	Oryza sativa	ric1. ras-related GTP binding protein possessing GTPase activity; This sequence comes from Fig. 1.
CAA98159.1	Z73931	Lotus japonicus	GTP-binding protein. RAB1B. rab1B.
BAA02115.1	D12547	Pisum sativum	GTP-binding protein.

CAA66447.1	X97853	Lotus japonicus	GTP-binding protein. RAB1A. rab1A.
AAD10389.1	U35026	Petunia x hybrida	Rab1-like small GTP-binding protein.
AAA80679.1	U38465	Lycopersicon esculentum	small GTP-binding protein. LeRab1B. ; Ypt1/Rab1A homolog LeRab1B.
BAB07961.1	AP002524	Oryza sativa	putative GTP-binding protein. P0406H10.17. contains ESTs D23874(R0480),AU031678(R0480).
CAA98176.1	Z73948	Lotus japonicus	GTP-binding protein. RAB8E. rab8E.
CAA89021.1	Z49152	Beta vulgaris	GTP-binding. small G protein.
CAA98172.1	Z73944	Lotus japonicus	GTP-binding protein. RAB8A. rab8A.
CAA04701.1	AJ001367	Daucus carota	small GTP-binding protein. Dc-Rab8.
CAA90080.1	Z49900	Pisum sativum	small GTP-binding protein.
AAD46405.1	AF096249	Lycopersicon esculentum	ethylene-responsive small GTP-binding protein. ER43.
CAA98174.1	Z73946	Lotus japonicus	GTP-binding protein. RAB8C. rab8C.
CAA90082.1	Z49902	Pisum sativum	small GTP-binding protein.
CAA49600.1	X69980	Lycopersicon esculentum	GTP-binding protein. ypt2.
CAA98175.1	Z73947	Lotus japonicus	GTP-binding protein. RAB8D. rab8D.
CAA90081.1	Z49901	Pisum sativum	small GTP-binding protein.
AAB17726.1	U38471	Brassica rapa	small GTP-binding protein rab. BRAB-1. small GTP-binding protein rab family.
AAA34251.1	L08128	Volvox carteri	GTP-binding protein. yptV2.
CAA98173.1	Z73945	Lotus japonicus	GTP-binding protein. RAB8B. rab8B.
CAA89049.1	Z49190	Beta vulgaris	GTP-binding. small G protein.
CAA98179.1	Z73951	Lotus japonicus	GTP-binding protein. RAB11C. rab11C.
AAA34253.1	L08130	Volvox carteri	GTP-binding protein. yptV4.

CAA98165.1	Z73937	Lotus japonicus	GTP-binding protein. RAB2A. rab2A.
AAA63902.1	U22433	Zea mays	GTP binding protein. rab2.
AAA90955.1	U32185	Glycine max	vesicular transport. guanine nucleotide regulatory protein. rab2. GTP-binding protein; soyrab.
SEQ ID NO: 628			
AAA87456.1	U22147	Hevea brasiliensis	beta-1,3-glucanase. HGN1. hydrolytic enzyme.
CAB38443.1	AJ133470	Hevea brasiliensis	beta-1,3-glucanase. hgn1.
AAG24921.1	AF311749	Hevea brasiliensis	beta-1,3-glucanase.
AAF44667.1	AF239617	Vitis vinifera	hydrolysis of 1,3-beta-D-glucosidic linkages in 1,3-beta-D-glucans. beta-1,3-glucanase. fungal pathogen defense-related protein.
AAA33648.1	L02212	Pisum sativum	beta-1,3-glucan hydrolysis. beta-1,3-glucanase. putative.
AAB41551.1	U27179	Medicago sativa subsp. sativa	acidic glucanase.
AAB24398.1	S51479	Pisum sativum	beta-1,3-glucanase. beta-1,3-glucanase. This sequence comes from Fig. 1B.
CAA37289.1	X53129	Phaseolus vulgaris	1,3,-beta-D-glucanase.
AAA34078.1	M63634	Nicotiana plumbaginifolia	regulator of beta(1,3)-glucanase. beta(1,3)-glucanase regulator.
AAA51643.1	M23120	Nicotiana plumbaginifolia	beta-glucanase precursor.
CAA30261.1	X07280	Nicotiana plumbaginifolia	beta-glucanase.
AAA03618.1	M80608	Lycopersicon esculentum	beta-1,3-glucanase.
AAC19114.1	AF067863	Solanum tuberosum	1,3-beta-glucan glucanohydrolase. glucanase.
AAA18928.1	U01901	Solanum tuberosum	catalyzes the hydrolysis of 1,3-beta-D-glucoside linkages in 1,3,-beta-D-glucans (such as laminarin). 1,3-beta-D-glucan glucanohydrolase; endo-1,3-beta-D-glucanase; 1,3-beta-glucanase (basic, class I). glub2. plant defense gene; induced expression in response to infection, elicitor, ethylene, wounding.
AAA63539.1	M60402	Nicotiana tabacum	glucan beta-1,3-glucanase. glucanase GLA.
AAA63540.1	M60403	Nicotiana tabacum	glucan-1,3-beta-glucosidase. glucanase GLB.

AAA88794.1	U01900	Solanum tuberosum	catalyzes the hydrolysis of 1,3-beta-D-glucoside linkages in 1,3,-beta-D-glucans (such as laminarin). 1,3-beta-D-glucan glucanohydrolase; endo-1,3-beta-D-glucanase; 1,3-beta-glucanase (basic, class I). gluB1. plant defense gene; induced expression in response to infection, elicitor, ethylene, wounding.
AAA63541.1	M59442	Nicotiana tabacum	basic beta-1,3-glucanase. glucanase.
AAB82772.2	AF001523	Musa acuminata	beta-1, 3-glucanase. similar to beta-1, 3-glucanase.
AAF08679.1	AF004838	Musa acuminata	beta-1,3-glucanase.
AAA19111.1	U01902	Solanum tuberosum	catalyzes the hydrolysis of 1,3-beta-D-glucoside linkages in 1,3,-beta-D-glucans (such as laminarin). 1,3-beta-D-glucan glucanohydrolase; endo-1,3-beta-D-glucanase; 1,3-beta-glucanase (basic, class I). gluB3. plant defense gene; induced expression in response to infection, elicitor, ethylene, wounding.
AAC04710.1	AF034106	Glycine max	beta-1,3-glucanase 1. SGlu1.
AAC04714.1	AF034113	Glycine max	beta-1,3-glucanase 8. SGlu8.
CAB91554.1	AJ277900	Vitis vinifera	beta 1-3 glucanase. gl.
AAA34082.1	M20620	Nicotiana tabacum	prepro-beta-1,3-glucanase precursor.
CAA03908.1	AJ000081	Citrus sinensis	glucan hydrolase. beta-1,3-glucanase. gns1.
AAB03501.1	U41323	Glycine max	beta-1,3-glucanase. SGN1.
AAA92013.1	U49454	Prunus persica	beta-1,3-glucanase. Gns1.
AAA33946.1	M37753	Glycine max	beta-1,3-endoglucanase (EC 3.2.1.39).
AAA63542.1	M59443	Nicotiana tabacum	acidic beta-1,3-glucanase. glucanase.
AAF34761.1	AF227953	Capsicum annuum	basic beta-1,3-glucanase. BGLU.
AAD33881.1	AF141654	Nicotiana tabacum	beta-1,3-glucanase. GGL4.
AAG34080.1	AF294849	Capsicum annuum	beta-1,3-glucanase-like protein.
AAF33405.1	AF230109	Populus x canescens	beta-1,3 glucanase. BGLUC.

AAD33880.1 AF141653 *Nicotiana tabacum*
beta-1,3-glucanase. GGL1.

CAA57255.1 X81560 *Nicotiana tabacum*
(1-)-beta-glucanase. Sp41a.

AAA34053.1 M60464 *Nicotiana tabacum*
beta-1,3-glucanase.

SEQ ID NO: 630

AAD37698.1 AF145729 *Oryza sativa*
homeodomain leucine zipper protein. Oshox5. transcription factor.

BAA05624.1 D26575 *Daucus carota*
transcriptional regulator. DNA-binding protein. homeodomain at nt 520-699; leucine zipper at nt 700-805.

AAF01765.1 AF184278 *Glycine max*
homeodomain-leucine zipper protein 57. Hdl57. transcription factor.

CAA64417.1 X94947 *Lycopersicon esculentum*
homeobox. VAHOX1.

BAA93465.1 AB028077 *Physcomitrella patens*
homeobox protein PpHB6. PpHB6. homeodomain-leucine zipper gene.

BAB18171.1 AB042769 *Zinnia elegans*
homeobox-leucine zipper protein. ZeHB3. full length.

BAA93460.1 AB028072 *Physcomitrella patens*
homeobox protein PpHB1. PpHB1. homeodomain-leucine zipper gene.

BAA93466.1 AB028078 *Physcomitrella patens*
homeobox protein PpHB7. PpHB7. homeodomain-leucine zipper gene.

BAA93461.1 AB028073 *Physcomitrella patens*
homeobox protein PpHB2. PpHB2. homeodomain-leucine zipper gene.

BAA05625.1 D26576 *Daucus carota*
transcriptional regulator. DNA-binding protein. homeodomain at nt 300-479; leucine zipper at nt 480-587.

BAA05622.1 D26573 *Daucus carota*
transcriptional regulator. DNA-binding protein. homeodomain at nt 585-764; leucine zipper at nt 765-851.

BAA93467.1 AB028079 *Physcomitrella patens*
homeobox protein PpHB8. PpHB8. homeodomain-leucine zipper gene.

BAA93464.1 AB028076 *Physcomitrella patens*
homeobox protein PpHB5. PpHB5. homeodomain-leucine zipper gene.

AAD37697.1 AF145728 *Oryza sativa*
homeodomain leucine zipper protein. Oshox4. transcription factor.

AAF01764.2 AF184277 *Glycine max*
homeodomain-leucine zipper protein 56. Hdl56. transcription factor.

BAA21017.1 D26578 *Daucus carota*
transcriptional regulator. DNA-binding protein. homeodomain at nt 761-940; leucine zipper at nt 941-1048.

BAB18168.1	AB042766	<i>Zinnia elegans</i> homeobox-leucine zipper protein. ZeHB7. 3'RACE product.
BAA93468.1	AB028080	<i>Physcomitrella patens</i> homeobox protein PpHB9. PpHB9. homeodomain-leucine zipper gene.
BAA05623.1	D26574	<i>Daucus carota</i> transcriptional regulator. DNA-binding protein. homeodomain at nt 498-677; leucine zipper at nt 678-785.
AAD37699.1	AF145730	<i>Oryza sativa</i> homeodomain leucine zipper protein. Oshox6. transcription factor.
AAD38144.1	AF139497	<i>Prunus armeniaca</i> DNA-binding protein. homeobox leucine zipper protein. HBLZP.
AAA63768.2	AF339748	<i>Helianthus annuus</i> homeobox-leucine zipper protein HAHB-4. Hahb-4.
BAA93463.1	AB028075	<i>Physcomitrella patens</i> homeobox protein PpHB4. PpHB4. homeodomain-leucine zipper gene.
CAA64491.1	X95193	<i>Pimpinella brachycarpa</i> transcription activator. homeobox-leucine zipper protein.
CAA64221.1	X94449	<i>Pimpinella brachycarpa</i> transcription activator. homeobox-leucine zipper protein. PHZ4.
CAA64152.1	X94375	<i>Pimpinella brachycarpa</i> transcription activator. homeobox-leucine zipper protein.
AAD37700.1	AF145731	<i>Oryza sativa</i> homeodomain leucine zipper protein. Oshox7. transcription factor.
AAD37695.1	AF145726	<i>Oryza sativa</i> homeodomain leucine zipper protein. Oshox2. transcription factor.
CAA06728.1	AJ005833	<i>Craterostigma plantagineum</i> transcription factor. homeodomain leucine zipper protein. hb-2.
CAA62608.1	X91212	<i>Lycopersicon esculentum</i> HD-ZIP protein. THOM1.
CAA63222.1	X92489	<i>Glycine max</i> transcription activator. homeobox-leucine zipper protein.
CAA65456.2	X96681	<i>Oryza sativa</i> transcription factor. DNA-binding protein. Oshox1. homeodomain leucine zipper gene.
AAF19980.1	AF211193	<i>Oryza sativa</i> homeodomain-leucine zipper transcription factor. Hox1. hox1.
SEQ ID NO: 631		
CAC19183.1	AJ291816	<i>Cicer arietinum</i> expansin.
AAD13633.1	AF059489	<i>Lycopersicon esculentum</i> expansin precursor. Exp5.
AAG13983.1	AF297522	<i>Prunus avium</i> expansin 2. Exp2. PruavExp2.

AAF35902.1	AF230333	<i>Zinnia elegans</i> expansin 3.
AAF32409.1	AF230276	<i>Triphysaria versicolor</i> alpha-expansin 3.
AAC96080.1	AF049353	<i>Nicotiana tabacum</i> involved in acid-growth response. alpha-expansin precursor. Nt-EXP4. cell wall protein.
AAG13982.1	AF297521	<i>Prunus avium</i> expansin 1. Exp1. PruavExp1.
AAC33529.1	U93167	<i>Prunus armeniaca</i> expansin. PA-Exp1.
AAF32411.1	AF230278	<i>Triphysaria versicolor</i> alpha-expansin 1.
AAF35901.1	AF230332	<i>Zinnia elegans</i> expansin 2.
AAF21101.1	AF159563	<i>Fragaria x ananassa</i> expansin. Exp2. ripening regulated.
BAB19676.1	AB029083	<i>Prunus persica</i> expansin. PchExp1.
AAD47901.1	AF085330	<i>Pinus taeda</i> expansin.
AAC33530.1	AF038815	<i>Prunus armeniaca</i> expansin. Exp2.
CAC19184.1	AJ291817	<i>Cicer arietinum</i> expansin.
AAB40635.1	U64891	<i>Pinus taeda</i> expansin. similar to Arabidopsis expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to Cucumis sativus expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.
AAG32921.1	AF184233	<i>Lycopersicon esculentum</i> expansin. Exp10.
AAD49956.1	AF167360	<i>Rumex palustris</i> expansin. EXP1.
AAB40637.1	U64893	<i>Pinus taeda</i> expansin. similar to Arabidopsis expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to Cucumis sativus expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.
AAB40634.1	U64890	<i>Pinus taeda</i> expansin. similar to Arabidopsis expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to Cucumis sativus expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.

AAB37746.1	U30382	Cucumis sativus	expansin S1 precursor. Cs-EXP1. similar to pollen allergen Lol pI, Lolium perenne, Swiss-Prot Accession Number P14946; former gene name CuExS1; expansin-29 (Ex29) protein.
AAB40636.1	U64892	Pinus taeda	expansin. similar to Arabidopsis expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to Cucumis sativus expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.
AAC39512.1	AF043284	Gossypium hirsutum	expansin. GhEX1. contains N-terminal signal peptide.
CAB43197.1	AJ239068	Lycopersicon esculentum	cell wall loosening enzyme. expansin2. exp2.
AAC64201.1	AF096776	Lycopersicon esculentum	expansin. LeEXP2.
AAC96081.1	AF049354	Nicotiana tabacum	involved in acid-growth response. alpha-expansin precursor. Nt-EXP5. cell wall protein.
CAB46492.1	AJ243340	Lycopersicon esculentum	expansin9. exp9.
AAF17570.1	AF202119	Marsilea quadrifolia	alpha-expansin. EXP1. Mq-EXP1.
AAB81662.1	U85246	Oryza sativa	expansin. Os-EXP4.
AAF62180.1	AF247162	Oryza sativa	alpha-expansin OsEXP5. cell wall loosening factor; expressed in internodes, leaves, coleoptiles, and roots.
AAB38074.1	U30477	Oryza sativa	induces extension (creep) in plant cell walls. expansin Os-EXP2. Os-EXP2. former gene name RiExB.
AAD13632.1	AF059488	Lycopersicon esculentum	expansin precursor. Exp4.
AAF32410.1	AF230277	Triphysaria versicolor	alpha-expansin 2.
AAG01875.1	AF291659	Striga asiatica	alpha-expansin 3. Exp3.
CAA04385.1	AJ000885	Brassica napus	Cell wall extension in plants. Expansin.
CAA06271.2	AJ004997	Lycopersicon esculentum	expansin18. exp18.
BAB32732.1	AB049406	Eustoma grandiflorum	expansin. Eg Expansin.
AAC63088.1	U82123	Lycopersicon esculentum	expansin. LeEXP1. fruit ripening regulated expansin.

AAF62182.1	AF247164	<i>Oryza sativa</i> alpha-expansin OsEXP7. cell wall loosening factor; expressed in internodes and leaves.
AAB37749.1	U30460	<i>Cucumis sativus</i> expansin S2 precursor. Cs-EXP2. similar to pollen allergen Lol pI, <i>Lolium perenne</i> , Swiss-Prot Accession Number P14946; former gene name CuExS2; expansin-30 (Ex30) protein.
AAG32920.1	AF184232	<i>Lycopersicon esculentum</i> expansin. Exp8.
CAC06433.1	AJ276007	<i>Festuca pratensis</i> expansin. exp2.
AAF62181.1	AF247163	<i>Oryza sativa</i> alpha-expansin OsEXP6. cell wall loosening factor; expressed in internodes and leaves.
AAC96079.1	AF049352	<i>Nicotiana tabacum</i> involved in acid-growth response. alpha-expansin precursor. Nt-EXP3. cell wall protein.
AAC96077.1	AF049350	<i>Nicotiana tabacum</i> involved in acid-growth response. alpha-expansin precursor. Nt-EXP1. cell wall protein.
BAA88200.1	AP000837	<i>Oryza sativa</i> EST AU078708(E60526) corresponds to a region of the predicted gene. Similar to expansin (U85246).
AAF17571.1	AF202120	<i>Regnellidium diphyllum</i> alpha-expansin. EXP1. Rd-EXP1.
AAC96078.1	AF049351	<i>Nicotiana tabacum</i> involved in acid-growth response. alpha-expansin precursor. Nt-EXP2. cell wall protein.
AAG01874.1	AF291658	<i>Striga asiatica</i> alpha-expansin 2. Exp2.
SEQ ID NO: 634		
AAF63205.1	AF245119	<i>Mesembryanthemum crystallinum</i> AP2-related transcription factor. CDBP. stress induced transcription factor.
BAA97122.1	AB016264	<i>Nicotiana sylvestris</i> ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf2.
BAA07321.1	D38123	<i>Nicotiana tabacum</i> ERF1. ethylene-responsive transcription factor.
AAG43545.1	AF211527	<i>Nicotiana tabacum</i> Avr9/Cf-9 rapidly elicited protein 1. ACRE1. similar to EREBP transcription factors.
BAA87068.1	AB035270	<i>Matricaria chamomilla</i> ethylene-responsive element binding protein1 homolog. McEREBP1.
BAA97124.1	AB016266	<i>Nicotiana sylvestris</i> ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf4.
AAC62619.1	AF057373	<i>Nicotiana tabacum</i> transcription factor. ethylene response element binding protein 1. EREBP1.
CAB93940.1	AJ238740	<i>Catharanthus roseus</i> putative transcription factor. AP2-domain DNA-binding protein. orca2.

AAK31279.1	AC079890	Oryza sativa	putative ethylene-responsive element binding protein. OSJNBb0089A17.16.
AAG60182.1	AC084763	Oryza sativa	putative ethylene-responsive element binding protein. OSJNBa0027P10.12.
CAB96900.1	AJ251250	Catharanthus roseus	transcription factor. AP2-domain DNA-binding protein. orca3.
CAB96899.1	AJ251249	Catharanthus roseus	transcription factor. AP2-domain DNA-binding protein. orca3.
CAC12822.1	AJ299252	Nicotiana tabacum	AP2 domain-containing transcription factor. ap2.
AAF23899.1	AF193803	Oryza sativa	transcription factor EREBP1. EREBP/AP2-like transcription factor.
AAF05606.1	AF190770	Oryza sativa	EREBP-like protein. tsh1. TSH1; induced by ethylene.
BAA97123.1	AB016265	Nicotiana sylvestris	ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf3.
BAA76734.1	AB024575	Nicotiana tabacum	ethylene responsive element binding factor.
BAB03248.1	AB037183	Oryza sativa	ERF protein transcriptional repressor. ethylene responsive element binding factor3. osERF3.
CAB93939.1	AJ238739	Catharanthus roseus	putative transcription factor. AP2-domain DNA-binding protein. orca1.
AAD00708.1	U91857	Stylosanthes hamata	ethylene-responsive element binding protein homolog. similar to EREBP1, -2, -3 and -4 proteins encoded by GenBank Accession Numbers D38123, D38126, D38124, and D38125 respectively.
AAG43548.1	AF211530	Nicotiana tabacum	Avr9/Cf-9 rapidly elicited protein 111A. ACRE111A. similar to EREBP transcription factors.
AAG43549.1	AF211531	Nicotiana tabacum	Avr9/Cf-9 rapidly elicited protein 111B. ACRE111B. similar to EREBP transcription factors.
AAK31271.1	AC079890	Oryza sativa	putative transcriptional factor. OSJNBb0089A17.22.
AAK01088.1	AF298230	Hordeum vulgare	CBF1-like protein BCBF1. BCBF1. AP2 domain protein; putative DRE binding factor.
AAC49567.1	U41466	Zea mays	Glossy15. Glossy15. AP2 DNA-binding domain protein; similar to the Arabidopsis floral homeotic gene APETALA2; maize AP2-domain regulator of leaf epidermal traits; homeotic regulator of leaf epidermal cell identity; allele: W64A; putative transcription factor.
SEQ ID NO: 635			
CAC19789.1	AJ251686	Catharanthus roseus	putative transcription factor. MYB-like DNA-binding protein. bpf-1.

CAA55693.1 X79086 Zea mays
initiator-binding protein. IBP2.

CAA55691.1 X79085 Zea mays
initiator binding protein. IBP1.

AAF97508.1 AF242298 Oryza sativa
telomere binding protein-1. TBP1.

SEQ ID NO: 636

CAB43505.1 AJ239051 Cicer arietinum
cytochrome P450. cyp81E2.

BAA22422.1 AB001379 Glycyrrhiza echinata
cytochrome P450. CYP81E1.

BAA74465.1 AB022732 Glycyrrhiza echinata
cytochrome P450. CYP Ge-31.

CAA10067.1 AJ012581 Cicer arietinum
cytochrome P450. cyp81E3.

CAB41490.1 AJ238439 Cicer arietinum
cytochrome P450 monooxygenase. cyp81E3v2.

BAA93634.1 AB025016 Lotus japonicus
cytochrome P450.

CAA04117.1 AJ000478 Helianthus tuberosus
fatty acid in-chain hydroxylase. cytochrome P450. CYP81B11. chimeric sequence (from 5'-
race).

CAA04116.1 AJ000477 Helianthus tuberosus
fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1c.

AAK38080.1 AF321856 Lolium rigidum
putative cytochrome P450.

AAK38079.1 AF321855 Lolium rigidum
putative cytochrome P450.

AAK38081.1 AF321857 Lolium rigidum
putative cytochrome P450.

AAC34853.1 AF082028 Hemerocallis hybrid cultivar
putative cyt P450-containing fatty acid hydroxylase. senescence-associated protein 3. SA3.
mRNA accumulates in senescing petals.

CAA65580.1 X96784 Nicotiana tabacum
cytochrome P450. hsr515.

CAB56742.1 AJ249800 Cicer arietinum
cytochrome P450 monooxygenase. cyp81E5.

AAA32913.1 M32885 Persea americana
cytochrome P-450LXXIA1 (cyp71A1).

BAA12159.1 D83968 Glycine max
Cytochrome P-450 (CYP93A1).

AAD56282.1 AF155332 Petunia x hybrida
flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.

CAA71515.1	Y10491	Glycine max putative cytochrome P450.
AAB94590.1	AF022461	Glycine max CYP82C1p. CYP82C1. cytochrome P450 monooxygenase.
CAA71516.1	Y10492	Glycine max putative cytochrome P450.
CAA64635.1	X95342	Nicotiana tabacum cytochrome P450. hsr515. hypersensitivity-related gene.
BAA13076.1	D86351	Glycine max cytochrome P-450 (CYP93A2).
AAG44132.1	AF218296	Pisum sativum cytochrome P450. P450 isolog.
AAG09208.1	AF175278	Pisum sativum wound-inducible P450 hydroxylase. CYP82A1.
AAC49188.2	U29333	Pisum sativum cytochrome P450 monooxygenase. CYP82. new cytochrome P450 family.
AAD38930.1	AF135485	Glycine max cytochrome P450 monooxygenase CYP93D1. CYP93E1.
CAA71876.1	Y10982	Glycine max putative cytochrome P450.
CAA70575.1	Y09423	Nepeta racemosa cytochrome P450. CYP71A5.
CAA70576.1	Y09424	Nepeta racemosa cytochrome P450. CYP71A6.
CAA71513.1	Y10489	Glycine max putative cytochrome P450.
CAA71877.1	Y10983	Glycine max putative cytochrome P450.
AAB94587.1	AF022458	Glycine max CYP98A2p. CYP98A2. cytochrome P450 monooxygenase.
AAC39454.1	AF014802	Eschscholzia californica (S)-N-methylcoclaurine 3'-hydroxylase. CYP82B1. cytochrome P-450-dependent monooxygenase; methyl jasmonate-inducible cytochrome P-450-dependent, homologous to wound-inducible CYP82A1 of Pisum sativum GenBank Accession Number U29333.
BAA92894.1	AB006790	Petunia x hybrida cytochrome P450. IMT-2.
BAA84072.1	AB028152	Torenia hybrida flavone synthase II. cytochrome P450. TFNS5.
BAA35080.1	AB015762	Nicotiana tabacum putative cytochrome P450. CYP82E1.
CAB56743.1	AJ249801	Cicer arietinum cytochrome P450 monooxygenase. cyp81E4.

AAB17562.1 U72654 *Eustoma grandiflorum*
flavonoid 3'5'-hydroxylase. F3'5'H. cytochrome P450; CYP75.

AAG34695.1 AF313492 *Matthiola incana*
putative cytochrome P450.

BAA74466.1 AB022733 *Glycyrrhiza echinata*
cytochrome P450. CYP Ge-51.

BAA22423.1 AB001380 *Glycyrrhiza echinata*
cytochrome P450. CYP93B1.

SEQ ID NO: 639

AAC06319.1 AF053084 *Malus x domestica*
putative cinnamyl alcohol dehydrogenase. CAD.

CAA61275.1 X88797 *Eucalyptus gunnii*
cinnamyl alcohol dehydrogenase. CAD1.

SEQ ID NO: 640

BAA92916.1 AP001539 *Oryza sativa*
EST C26826(C50159) corresponds to a region of the predicted gene. Similar to *Arabidopsis thaliana* chromosome II BAC F13A10; putative ARF1 family auxin responsive transcription factor. (AC006418).

AAK21342.1 AC024594 *Oryza sativa*
putative transcription factor. OSJNBa0093B11.2.

AAG43286.1 AF140228 *Oryza sativa*
auxin response factor 1.

SEQ ID NO: 641

CAC24691.1 AJ132363 *Brassica juncea*
efflux carrier of polar auxin transport. pina.

AAG17172.1 AF190881 *Populus tremula x Populus tremuloides*
PIN1-like auxin transport protein. ppl1.

AAC39514.1 AF056027 *Oryza sativa*
auxin transport protein REH1. REH1. potential membrane protein.

SEQ ID NO: 642

AAG22044.1 AF305783 *Pisum sativum*
apyrase 2. apy2. phosphatase.

AAF00610.1 AF156781 *Dolichos biflorus*
apyrase. apyrase-2.

AAG32959.1 AF207687 *Glycine soja*
apyrase GS50.

AAG32960.1 AF207688 *Glycine soja*
apyrase GS52.

AAF00609.1 AF156780 *Lotus japonicus*
apyrase. nod factor binding lectin-nucleotide phosphohydrolase. LNP.

AAD31285.1 AF139807 *Dolichos biflorus*
apyrase. nod factor binding lectin-nucleotide phosphohydrolase. LNP.

AAF00611.1	AF156782	Medicago sativa apyrase. nod factor binding lectin-nucleotide phosphohydrolase. LNP.
AAK15160.1	AF288132	Medicago truncatula putative apyrase. apy1. nucleotide phosphohydrolase; Mtapy1.
BAB18896.1	AB038669	Pisum sativum apyrase.
BAB18895.1	AB038668	Pisum sativum apyrase.
BAB18894.1	AB038555	Pisum sativum apyrase H-type.
BAB18893.1	AB038554	Pisum sativum apyrase S-type.
BAB18900.1	AB027614	Pisum sativum apyrase.
BAB40230.1	AB027613	Pisum sativum S-type apyras. ATP diphosphohydrolase (apyrase) S-type.
BAB18890.1	AB023621	Pisum sativum apyrase S-type. ATP diphosphohydrolase (apyrase) S-type.
BAA75506.1	AB022319	Pisum sativum apyrase. cytoskeleton associated.
BAA89275.1	AB027616	Pisum sativum apyrase.
BAB40231.1	AB027615	Pisum sativum S-type apyrase. ATP diphosphohydrolase (apyrase) S-type.
AAB02720.1	U58597	Solanum tuberosum catalyzes the hydrolysis of phosphoanhydride bonds of nucleoside tri- and di- phosphates in the presence of divalent cations. ATP-diphosphohydrolase. RROP1. apyrase, Ecto-ATPase, E-type ATPase; NTP-diphosphohydrolase.
AAK15161.1	AF288133	Medicago truncatula putative apyrase. apy4. nucleotide phosphohydrolase; Mtapy4.
BAB18891.1	AB030444	Pisum sativum apyrase. ATP diphosphohydrolase, (EC 3.6.1.5) this sequence is reported in Acc#:AB022319.
BAB18892.1	AB030445	Pisum sativum apyrase. ATP diphosphohydrolase, EC 3.6.1.5 this sequence is reported in Acc#:AB022319, Acc#:AB027613.
SEQ ID NO: 645		
AAG22044.1	AF305783	Pisum sativum apyrase 2. apy2. phosphatase.
AAF00610.1	AF156781	Dolichos biflorus apyrase. apyrase-2.
AAG32959.1	AF207687	Glycine soja apyrase GS50.

AAG32960.1	AF207688	Glycine soja apyrase GS52.
AAD31285.1	AF139807	Dolichos biflorus apyrase. nod factor binding lectin-nucleotide phosphohydrolase. LNP.
AAK15160.1	AF288132	Medicago truncatula putative apyrase. apy1. nucleotide phosphohydrolase; Mtapy1.
AAF00609.1	AF156780	Lotus japonicus apyrase. nod factor binding lectin-nucleotide phosphohydrolase. LNP.
BAB18896.1	AB038669	Pisum sativum apyrase.
BAB18895.1	AB038668	Pisum sativum apyrase.
BAB18894.1	AB038555	Pisum sativum apyrase H-type.
BAB18893.1	AB038554	Pisum sativum apyrase S-type.
BAB18900.1	AB027614	Pisum sativum apyrase.
BAB40230.1	AB027613	Pisum sativum S-type apyras. ATP diphosphohydrolase (apyrase) S-type.
BAB18890.1	AB023621	Pisum sativum apyrase S-type. ATP diphosphohydrolase (apyrase) S-type.
BAA75506.1	AB022319	Pisum sativum apyrase. cytoskeleton associated.
AAF00611.1	AF156782	Medicago sativa apyrase. nod factor binding lectin-nucleotide phosphohydrolase. LNP.
BAA89275.1	AB027616	Pisum sativum apyrase.
BAB40231.1	AB027615	Pisum sativum S-type apyrase. ATP diphosphohydrolase (apyrase) S-type.
AAB02720.1	U58597	Solanum tuberosum catalyzes the hydrolysis of phosphoanhydride bonds of nucleoside tri- and di- phosphates in the presence of divalent cations. ATP-diphosphohydrolase. RROP1. apyrase, Ecto-ATPase, E-type ATPase; NTP-diphosphohydrolase.
AAK15161.1	AF288133	Medicago truncatula putative apyrase. apy4. nucleotide phosphohydrolase; Mtapy4.
BAB18891.1	AB030444	Pisum sativum apyrase. ATP diphosphohydrolase, (EC 3.6.1.5) this sequence is reported in Acc#:AB022319.
BAB18892.1	AB030445	Pisum sativum apyrase. ATP diphosphohydrolase, EC 3.6.1.5 this sequence is reported in Acc#:AB022319, Acc#:AB027613.

SEQ ID NO: 646

AAB80947.1 AF022915 *Triticum aestivum*
ornithine/acetylornithine aminotransferase.

CAA69936.1 Y08680 *Alnus glutinosa*
acetylornithine aminotransferase. ag118.

AAK11219.1 AF324485 *Oryza sativa*
aminotransferase-like protein.

AAG09278.1 AF177590 *Vitis vinifera*
ornithine aminotransferase.

AAC78480.1 AF085149 *Capsicum chinense*
putative aminotransferase. pyridoxal phosphate dependent.

AAA02916.1 L08400 *Vigna aconitifolia*
production of pyrroline-5-carboxylate by deamination of ornithine. ornithine
aminotransferase.

AAB59330.1 M31545 *Hordeum vulgare*
glutamate 1-semialdehyde aminotransferase. GSA. precursor.

AAA18861.1 U03632 *Chlamydomonas reinhardtii*
glutamate-1-semialdehyde aminotransferase. gsa.

AAA33968.1 L12453 *Glycine max*
catalyzes 5-aminolevulinic acid formation from GSA. glutamate 1-semialdehyde
aminotransferase. Gsa. putative.

AAC48996.1 U20260 *Glycine max*
converts GSA to 5-aminolevulinic acid. glutamate 1-semialdehyde aminotransferase. Gsa1.

SEQ ID NO: 650

AAF66982.1 AF247646 *Zea mays*
transposase. similar to Mutator family transposases.

SEQ ID NO: 652

AAB41812.1 L36158 *Medicago sativa*
peroxidase. pxdD. amino acid feature: conserved domains, aa 120 .. 126, 188 .. 195; amino
acid feature: heme-binding domain, aa 63 .. 68.

CAA71495.1 Y10469 *Spinacia oleracea*
peroxidase. prxr8.

CAA09881.1 AJ011939 *Trifolium repens*
peroxidase. prx2.

CAA62228.1 X90695 *Medicago sativa*
peroxidase2. prx2.

AAA98491.1 L36981 *Petroselinum crispum*
anionic peroxidase.

BAB39281.1 AP002971 *Oryza sativa*
putative peroxidase. P0537A05.10. contains ESTs D24657(R2329), AU082066(R2329).

AAB02926.1 U59284 *Linum usitatissimum*
peroxidase. FLXPER3.

BAA77387.1 AB024437 *Scutellaria baicalensis*
peroxidase 1.

CAA66037.1	X97351	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
CAA71488.1	Y10462	Spinacia oleracea peroxidase. prxr1.
BAA01950.1	D11337	Vigna angularis peroxidase.
BAA14143.1	D90115	Armoracia rusticana peroxidase isozyme.
CAA71490.1	Y10464	Spinacia oleracea peroxidase. prxr3.
CAB94692.1	AJ242742	Ipomoea batatas Removal of H ₂ O ₂ , oxidation of toxic reductants, defence response toward wounding. peroxidase. pod.
BAA92497.1	AP001383	Oryza sativa ESTs AU081576(R0541),AU032412(R4029) correspond to a region of the predicted gene. Similar to peroxidase ATP18a. (X98804).
AAC36707.1	AF078691	Manihot esculenta peroxidase.
BAA92422.1	AP001366	Oryza sativa ESTs AU081576(R0541),AU032412(R4029) correspond to a region of the predicted gene. Similar to A.thaliana mRNA for peroxidase ATP18a. (X98804).
CAA62226.1	X90693	Medicago sativa peroxidase1B. prx1B.
AAF63024.1	AF244921	Spinacia oleracea hydrogen peroxide catabolism. peroxidase prx12 precursor. type III peroxidase.
AAA32676.1	M37637	Arachis hypogaea cationic peroxidase. PNC2.
BAA11853.1	D83225	Populus nigra peroxidase.
CAC21393.1	AJ401276	Zea mays peroxidase. pox3.
AAA65636.1	L13653	Lycopersicon esculentum peroxidase. TPX2.
CAB67121.1	Y19023	Lycopersicon esculentum peroxidase. cevi-1.
CAA62227.1	X90694	Medicago sativa peroxidase1C. prx1C.
CAA50597.1	X71593	Lycopersicon esculentum peroxidase. CEVI-1.
AAD37376.1	AF145350	Glycine max peroxidase. Prx4.
AAB67737.1	L77080	Stylosanthes humilis cationic peroxidase.

CAA71489.1	Y10463	Spinacia oleracea peroxidase. prxr2.
CAA71496.1	Y10470	Spinacia oleracea peroxidase. prxr9.
CAA71494.1	Y10468	Spinacia oleracea peroxidase. prxr7.
BAA06334.1	D30652	Populus kitakamiensis peroxidase.
CAA66034.1	X97348	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
BAA94962.1	AB042103	Asparagus officinalis peroxidase. AspPOX1.
CAA80502.1	Z22920	Spirodela polyrrhiza peroxidase.
CAA66035.1	X97349	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
BAA11852.1	D83224	Populus nigra peroxidase.
CAA66036.1	X97350	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
BAA07241.1	D38051	Populus kitakamiensis peroxidase. prxA4a.
AAD11481.1	U51191	Glycine max peroxidase precursor. sEPa1.
AAC98519.1	AF007211	Glycine max peroxidase precursor. GMIPER1. pathogen-induced.
AAA32973.1	M73234	Hordeum vulgare peroxidase BP 1. Prx5.
AAB47602.1	L07554	Linum usitatissimum peroxidase. FLXPER1.
AAB41810.1	L36156	Medicago sativa peroxidase. pxdA. amino acid feature: conserved motifs, aa 181 .. 188; amino acid feature: heme-binding domain, aa 60 .. 65.
AAF63027.1	AF244924	Spinacia oleracea hydrogen peroxide catabolism. peroxidase prx15 precursor. type III peroxidase.
AAA34108.1	J02979	Nicotiana tabacum lignin-forming peroxidase precursor (EC 1.11.1.7).
AAD43561.1	AF155124	Gossypium hirsutum bacterial-induced peroxidase precursor. Perx_Goshiko.
SEQ ID NO: 653		

AAB97617.1	U83687	<i>Apium graveolens</i>	NADPH-dependent mannose 6-phosphate reductase. m6pr. aldo-keto reductase; similar to aldose 6-phosphate reductase also known as NADP-sorbitol-6-phosphate dehydrogenase encoded by GenBank Accession Number D11080.
BAA01853.1	D11080	<i>Malus x domestica</i>	NADP-dependent D-sorbitol-6-phosphate dehydrogenase. S6PDH.
AAC97607.1	AF057134	<i>Malus x domestica</i>	synthesizes sorbitol, a major photosynthetic product in many members of the Rosaceae family. NADP-dependent sorbitol 6-phosphate dehydrogenase. S6PDH.
SEQ ID NO: 654			
BAA82556.1	AB030083	<i>Populus nigra</i>	lectin-like protein kinase. PnLPK.
AAB61708.1	U93048	<i>Daucus carota</i>	somatic embryogenesis receptor-like kinase. SERK.
BAB19337.1	AP003044	<i>Oryza sativa</i>	putative protein kinase. P0038C05.10. contains ESTs AU056335(S20481),AU056336(S20481).
AAK21965.1	AY028699	<i>Brassica napus</i>	receptor protein kinase PERK1.
BAB39873.1	AP002882	<i>Oryza sativa</i>	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
AAB93834.1	U82481	<i>Zea mays</i>	KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
BAB18292.1	AP002860	<i>Oryza sativa</i>	putative receptor-like protein kinase. P0409B08.19.
AAK00425.1	AC069324	<i>Oryza sativa</i>	Putative protein kinase. OSJNBa0071K19.11.
AAD21872.1	AF078082	<i>Phaseolus vulgaris</i>	receptor-like protein kinase homolog RK20-1.
AAC23542.1	U20948	<i>Ipomoea trifida</i>	receptor protein kinase. IRK1.
CAA73134.1	Y12531	<i>Brassica oleracea</i>	serine/threonine kinase. BRLK.
CAB51480.1	Y14600	<i>Sorghum bicolor</i>	putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.
AAG59657.1	AC084319	<i>Oryza sativa</i>	putative protein kinase. OSJNBa0004B24.20.
BAB16871.1	AP002537	<i>Oryza sativa</i>	putative protein kinase APK1A <i>Arabidopsis thaliana</i> . P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).

CAB51834.1	00069	Oryza sativa	11332.5. contains eukaryotic protein kinase domain PF.
BAA94509.1	AB041503	Populus nigra	protein kinase 1. PnPK1.
AAG16628.1	AY007545	Brassica napus	protein serine/threonine kinase BNK1.
BAA87853.1	AP000816	Oryza sativa	EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
BAB03429.1	AP002817	Oryza sativa	EST C22619(S11214) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).
BAB07999.1	AP002525	Oryza sativa	putative protein kinase. P0462H08.22. contains EST C22619(S11214).
BAB21240.1	AP002953	Oryza sativa	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
BAA92954.1	AP001551	Oryza sativa	Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).
BAA94510.1	AB041504	Populus nigra	protein kinase 2. PnPK2.
AAG03090.1	AC073405	Oryza sativa	Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).
AAF91322.1	AF244888	Glycine max	receptor-like protein kinase 1. RLK1. GmRLK1.
BAA94517.1	AP001800	Oryza sativa	Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAB07905.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.13.
CAB51836.1	AJ243961	Oryza sativa	Putative Ser/Thr protein kinase. 11332.7.
BAA78764.1	AB023482	Oryza sativa	ESTs C98382(C2985),D22444(C11129) correspond to a region of the predicted gene.; Similar to Arabidopsis thaliana APK1 gene for protein tyrosine-serine-threonine kinase.(D12522).
AAA33915.1	L27821	Oryza sativa	receptor type serine/threonine kinase. protein kinase.
AAF91323.1	AF244889	Glycine max	receptor-like protein kinase 2. RLK2. GmRLK2.
CAA67145.1	X98520	Brassica oleracea	receptor-like kinase. SFR2.
CAA73133.1	Y12530	Brassica oleracea	serine /threonine kinase. ARLK.
AAF91324.1	AF244890	Glycine max	receptor-like protein kinase 3. RLK3. GmRLK3.

CAA74661.1	Y14285	Brassica oleracea	SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.
BAA92953.1	AP001551	Oryza sativa	Similar to Arabidopsis thaliana chromosome 4 BAC clone F10M6 ; S-receptor kinase -like protein. (AL021811).
BAB40094.1	AP003210	Oryza sativa	putative receptor protein kinase. OSJNBa0010K01.7.
AAF43496.1	AF131222	Lophopyrum elongatum	protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.
AAK11674.1	AF339747	Lophopyrum elongatum	protein kinase. ESI47.
BAB07906.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.14.
BAA94516.1	AP001800	Oryza sativa	Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
CAB41878.1	Y18259	Brassica oleracea	SRK5 protein. SRK5. receptor-like kinase.
BAA23676.1	AB000970	Brassica rapa	receptor kinase 1. BcRK1.
CAB41879.1	Y18260	Brassica oleracea	SRK15 protein. SRK15. receptor-like kinase.
SEQ ID NO: 655			
AAD21872.1	AF078082	Phaseolus vulgaris	receptor-like protein kinase homolog RK20-1.
CAA73134.1	Y12531	Brassica oleracea	serine/threonine kinase. BRLK.
CAA67145.1	X98520	Brassica oleracea	receptor-like kinase. SFR2.
CAA73133.1	Y12530	Brassica oleracea	serine /threonine kinase. ARLK.
AAB93834.1	U82481	Zea mays	KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
BAA23676.1	AB000970	Brassica rapa	receptor kinase 1. BcRK1.
AAC23542.1	U20948	Ipomoea trifida	receptor protein kinase. IRK1.
CAB41879.1	Y18260	Brassica oleracea	SRK15 protein. SRK15. receptor-like kinase.

CAA74662.1	Y14286	Brassica oleracea	SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
CAB89179.1	AJ245479	Brassica napus subsp. napus	ser /thr kinase. S-locus receptor kinase. srk.
AAA33008.1	M97667	Brassica napus	serine/threonine kinase receptor.
AAA62232.1	U00443	Brassica napus	S-receptor kinase. protein contains an immunoglobulin-like domain.
CAA74661.1	Y14285	Brassica oleracea	SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.
AAA33000.1	M76647	Brassica oleracea	receptor protein kinase. SKR6.
CAA79355.1	Z18921	Brassica oleracea	S-receptor kinase-like protein.
CAB41878.1	Y18259	Brassica oleracea	SRK5 protein. SRK5. receptor-like kinase.
BAA07576.1	D38563	Brassica rapa	receptor protein kinase SRK8.
BAA06285.1	D30049	Brassica rapa	S-receptor kinase SRK9.
BAA21132.1	D88193	Brassica rapa	S-receptor kinase. SRK9 (B.c).
BAA07577.2	D38564	Brassica rapa	receptor protein kinase SRK12.
BAA92836.1	AB032473	Brassica oleracea	S18 S-locus receptor kinase. SRK18.
BAB21001.1	AB054061	Brassica rapa	S locus receptor kinase. SRK22.
BAA92837.1	AB032474	Brassica oleracea	S60 S-locus receptor kinase. SRK60.
BAB18292.1	AP002860	Oryza sativa	putative receptor-like protein kinase. P0409B08.19.
AAD52097.1	AF088885	Nicotiana tabacum	receptor-like kinase CHRK1. Chrk1.
BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
AAK21965.1	AY028699	Brassica napus	receptor protein kinase PERK1.
AAA33915.1	L27821	Oryza sativa	receptor type serine/threonine kinase. protein kinase.

AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.
BAA94529.2	AP001800	Oryza sativa	Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAB16871.1	AP002537	Oryza sativa	putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
AAF34428.1	AF172282	Oryza sativa	receptor-like protein kinase. DUPR11.18.
AAG03090.1	AC073405	Oryza sativa	Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).
BAB21240.1	AP002953	Oryza sativa	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
BAA87853.1	AP000816	Oryza sativa	EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
BAA94516.1	AP001800	Oryza sativa	Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAB07905.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.13.
BAB07906.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.14.
SEQ ID NO: 657			
AAF43869.1	AF166114	Chloroplast Mesostigma viride	probable transport protein. cysA.
BAB17113.1	AP002866	Oryza sativa	putative white protein; ATP-binding cassette transporter. P0410E01.34.
BAA57907.1	AB001684	Chlorella vulgaris	sulfate transport system permease protein. cysA.
AAD54843.1	AF137379	Chloroplast Nephroselmis olivacea	probable transport protein. cysA.
BAA90508.1	AP001111	Oryza sativa	similar to ABC transporter of Arabidopsis thaliana (AC004697).
BAA90507.1	AP001111	Oryza sativa	similar to ABC transporter of Arabidopsis thaliana (AC004697).
BAA83352.1	AP000391	Oryza sativa	ESTs AU067992(C11433),AU077424(C11433) correspond to a region of the predicted gene.; Similar to ABC transporter-7 (U43892).
AAG49003.1	AY013246	Hordeum vulgare	putative ABC transporter. 635P2.4b; GC splice donor confirmed by cDNA alignment and comparative sequence.
AAD10836.1	U52079	Solanum tuberosum	P-glycoprotein. pmdrl. binds ATP; ATPase; transporter; transmembrane protein.

BAA96612.1	AP002482	Oryza sativa	Similar to Arabidopsis thaliana chromosome 2, BAC F14M4 ; putative ABC transporter (AC004411).
BAB40032.1	AP003046	Oryza sativa	putative ABC transporter. P0445D12.3.
AAG45492.1	AY013245	Oryza sativa	36I5.4. putative ABC transporter; GC splice donor confirmed by cDNA alignment and comparative sequence.
AAG49002.1	AY013246	Hordeum vulgare	putative ABC transporter. 635P2.4a; GC splice donor confirmed by cDNA and comparative sequencing.
BAB21275.1	AP002844	Oryza sativa	putative ABC transporter protein. P0410E03.6.
BAB21273.1	AP002844	Oryza sativa	putative ABC transporter protein. P0410E03.4.
CAA94437.1	Z70524	Spirodela polyrrhiza	multidrug resistance protein. PDR5-like ABC transporter.
BAB21276.1	AP002844	Oryza sativa	putative ABC transporter protein. P0410E03.7. contains EST D22472(C1173).
BAB21279.1	AP002844	Oryza sativa	putative ABC transporter protein. P0410E03.10. contains ESTs AU065360(R3463),AU101680(R3463).
SEQ ID NO: 658			
AAD10386.1	U72255	Oryza sativa	beta-1,3-glucanase precursor. Gns9.
BAA89481.1	AB029462	Salix gilgiana	beta-1,3-glucanase. SgGN1.
CAB85903.1	AJ251646	Pisum sativum	hydrolysis of beta-1,3 conjugated glucans. beta-1,3 glucanase. gns2.
CAA49513.1	X69887	Brassica napus	beta-1,3-glucanase homologue.
AAA90953.1	U30323	Triticum aestivum	beta 1,3-glucanase. Glc1.
BAB19363.1	AP002542	Oryza sativa	putative beta-1,3-glucanase. P0679C08.2.
CAA82271.1	Z28697	Nicotiana tabacum	beta-1,3-glucanase.
CAA30261.1	X07280	Nicotiana plumbaginifolia	beta-glucanase.
AAA51643.1	M23120	Nicotiana plumbaginifolia	beta-glucanase precursor.
AAA34078.1	M63634	Nicotiana plumbaginifolia	regulator of beta(1,3)-glucanase. beta(1,3)-glucanase regulator.

AAB82772.2	AF001523	Musa acuminata	beta-1, 3-glucanase. similar to beta-1, 3-glucanase.
AAF08679.1	AF004838	Musa acuminata	beta-1,3-glucanase.
CAB71021.1	AJ271598	Hieracium piloselloides	putative role in callose degradation. putative beta-1,3-glucanase. gluc.
AAD10383.1	U72252	Oryza sativa	beta-1,3-glucanase precursor. Gns6.
AAD28732.1	AF112965	Triticum aestivum	beta-1,3-glucanase precursor. Glb3.
BAB40807.1	AB052291	Pyrus pyrifolia	catalyzing the hydrolysis of 1,3-beta-glucosyl linkages. endo-1,3-beta-glucanase-like protein. bgn-1. Amino acid alignment of the protein(BGN-1) encoded by pear pollen bgn-1 with barley endo-1,3-beta-glucanase(GII. accession number: pdb/1GHS-B/2.3/2/306/N/)(40% identity) and their hydrophobic cluster analysis(HCA)(a overall HCA homology score of 87.1%) showed that it was most likely that the bgn-1 encoded a endo-1,3-beta-glucanase. A higher identity(59.3%) was found between BGN-1 and a putative pea endo-1,3-beta-glucanase (accession number: dad/AJ251646-1).
AAA63539.1	M60402	Nicotiana tabacum	glucan beta-1,3-glucanase. glucanase GLA.
AAA63541.1	M59442	Nicotiana tabacum	basic beta-1,3-glucanase. glucanase.
AAA63540.1	M60403	Nicotiana tabacum	glucan-1,3-beta-glucosidase. glucanase GLB.
AAA32939.1	M62907	Hordeum vulgare	hydrolysis of beta-(1-3)-glucan. (1-3)-beta-glucanase. cBGL32.
AAC14399.1	AF030771	Hordeum vulgare	beta-1,3-glucanase 2. BGL32.
AAA87456.1	U22147	Hevea brasiliensis	beta-1,3-glucanase. HGN1. hydrolytic enzyme.
BAA77784.1	AB027429	Oryza sativa	beta-1,3-glucanase.
BAA77785.1	AB027430	Oryza sativa	beta-1,3-glucanase.
CAB91554.1	AJ277900	Vitis vinifera	beta 1-3 glucanase. gl.
AAD10381.1	U72250	Oryza sativa	beta-1,3-glucanase precursor. Gns4.
AAA33946.1	M37753	Glycine max	beta-1,3-endoglucanase (EC 3.2.1.39).
AAD33881.1	AF141654	Nicotiana tabacum	beta-1,3-glucanase. GGL4.

AAB86541.1	AF030166	Oryza sativa	glucanase. glu1.
AAD10384.1	U72253	Oryza sativa	beta-1,3-glucanase precursor. Gns7.
CAB38443.1	AJ133470	Hevea brasiliensis	beta-1,3-glucanase. hgn1.
AAB03501.1	U41323	Glycine max	beta-1,3-glucanase. SGN1.
AAA18928.1	U01901	Solanum tuberosum	catalyzes the hydrolysis of 1,3-beta-D-glucoside linkages in 1,3,-beta-D-glucans (such as laminarin). 1,3-beta-D-glucan glucanohydrolase; endo-1,3-beta-D-glucanase; 1,3-beta-glucanase (basic, class I). glub2. plant defense gene; induced expression in response to infection, elicitor, ethylene, wounding.
AAA88794.1	U01900	Solanum tuberosum	catalyzes the hydrolysis of 1,3-beta-D-glucoside linkages in 1,3,-beta-D-glucans (such as laminarin). 1,3-beta-D-glucan glucanohydrolase; endo-1,3-beta-D-glucanase; 1,3-beta-glucanase (basic, class I). gluB1. plant defense gene; induced expression in response to infection, elicitor, ethylene, wounding.
AAC19114.1	AF067863	Solanum tuberosum	1,3-beta-glucan glucanohydrolase. glucanase.
AAG24921.1	AF311749	Hevea brasiliensis	beta-1,3-glucanase.
CAA03908.1	AJ000081	Citrus sinensis	glucan hydrolase. beta-1,3-glucanase. gns1.
CAA37289.1	X53129	Phaseolus vulgaris	1,3,-beta-D-glucanase.
CAA57255.1	X81560	Nicotiana tabacum	(1-)-beta-glucanase. Sp41a.
SEQ ID NO: 659			
AAB65776.1	U97521	Vitis vinifera	class IV endochitinase. VvChi4A.
AAB65777.1	U97522	Vitis vinifera	class IV endochitinase. VvChi4B.
BAA03751.1	D16223	Oryza sativa	endochitinase. Cht-3.
CAA30142.1	X07130	Solanum tuberosum	endochitinase.
BAA03749.1	D16221	Oryza sativa	endochitinase. Cht-1.
SEQ ID NO: 660			
AAF07221.1	AF072519	Nicotiana tabacum	centrin. CEN1. caltractin; EF-hand domain calcium-binding protein.

AAF07222.1	AF072520	Nicotiana tabacum	centrin. CEN2. caltractin; EF-hand domain calcium-binding protein.
CAA49153.1	X69220	Scherffelia dubia	caltractin.
AAC04626.1	U92973	Marsilea vestita	calcium-binding protein. centrin. MvCen1. caltractin.
AAB67855.1	U53812	Dunaliella salina	caltractin-like protein.
CAA41039.1	X57973	Chlamydomonas reinhardtii	caltractin.
CAA31163.1	X12634	Chlamydomonas reinhardtii	caltractin (AA 1 - 169).
SEQ ID NO: 664			
BAB16432.1	AB041520	Nicotiana tabacum	WRKY transcription factor Nt-SubD48. Nt-SubD48.
AAC49528.1	U56834	Petroselinum crispum	DNA-binding. WRKY3. WRKY-type DNA-binding protein.
AAD27591.1	AF121354	Petroselinum crispum	binds sequence specifically to W Boxes (TTGACC). transcription factor. WRKY3. sequence specific DNA-binding protein.
AAD32676.1	AF140553	Avena sativa	DNA-binding protein WRKY3. wrky3. putative transcription factor.
BAA77358.1	AB020023	Nicotiana tabacum	WRKY domain Zn-finger type DNA-binding protein. DNA-binding protein NtWRKY3.
AAG46150.1	AC018727	Oryza sativa	putative DNA-binding protein. OSJNBa0056G17.18.
BAB40073.1	AP003074	Oryza sativa	putative WRKY DNA binding protein. OSJNBa0004G10.20. contains EST C26525(C12525).
BAB18313.1	AP002865	Oryza sativa	putative WRKY DNA binding protein. P0034C11.1. contains EST C26525(C12525).
AAD38283.1	AC007789	Oryza sativa	putative WRKY DNA binding protein. OSJNBa0049B20.9.
BAA77383.1	AB020590	Nicotiana tabacum	transcription factor NtWRKY2.
BAA82107.1	AB022693	Nicotiana tabacum	transcription factor. NtWRKY1.
CAA88326.1	Z48429	Avena fatua	binds conserved cis-element from cereal alpha-Amy2 promoters. DNA-binding protein.
AAD32677.1	AF140554	Avena sativa	DNA-binding protein WRKY1. wrky1. putative transcription factor.
AAD55974.1	AF121353	Petroselinum crispum	zinc-finger type transcription factor WRKY1. WRKY1.

AAC49529.1	U58540	Petroselinum crispum	WRKY2. Contains two WRKY domains; WRKY-type DNA-binding protein.
AAC49527.1	U48831	Petroselinum crispum	WRKY1. contains two WRKY domains; WRKY-type DNA-binding protein; sequence-specific DNA-binding protein.
AAC31956.1	AF080595	Pimpinella brachycarpa	zinc finger protein. ZFP1. WRKY1.
BAA86031.1	AB026890	Nicotiana tabacum	transcription factor NtWRKY4.
AAD16139.1	AF096299	Nicotiana tabacum	DNA-binding protein 2. WRKY2. transcription factor.
AAF23898.1	AF193802	Oryza sativa	zinc finger transcription factor WRKY1.
AAD16138.1	AF096298	Nicotiana tabacum	DNA-binding protein 1. WRKY1. transcription factor.
AAC37515.1	L44134	Cucumis sativus	SPF1-like DNA-binding protein.
AAG35658.1	AF204925	Petroselinum crispum	transcription factor WRKY4. WRKY4. binds to W box (TTGACC) elements.
CAA88331.1	Z48431	Avena fatua	binds conserved cis-element from cereal alpha-Amy2 promoters. DNA-binding protein.
BAB19075.1	AP002744	Oryza sativa	putative DNA-binding protein homolog. P0006C01.17.
BAB19096.1	AP002839	Oryza sativa	putative DNA-binding protein homolog. P0688A04.2.
AAK16170.1	AC079887	Oryza sativa	putative DNA binding protein. OSJNBa0040E01.4.
AAK16171.1	AC079887	Oryza sativa	putative DNA-binding protein. OSJNBa0040E01.10.
AAG35659.1	AF204926	Petroselinum crispum	transcription factor WRKY5. WRKY5. binds to W box (TTGACC) elements.
CAB97004.1	AJ278507	Solanum tuberosum	putative transcription factor. WRKY DNA binding protein. WRKY1.
AAF61864.1	AF193771	Nicotiana tabacum	DNA-binding protein 4. WRKY4. transcription factor.
BAA87069.1	AB035271	Matricaria chamomilla	elicitor-induced DNA-binding protein homolog. McWRKY1.
AAF61863.1	AF193770	Nicotiana tabacum	DNA-binding protein 3. WRKY3. transcription factor.
SEQ ID NO: 665			
AAD02558.1	AF049933	Petunia x hybrida	PGPS/NH17. PGPS/NH17. protein sec61 gamma subunit homolog; protein transport to ER.
SEQ ID NO: 667			

AAD51623.1 AF169020 Glycine max
seed maturation protein PM35. PM35. similar to Phaseolus vulgaris putative osmoprotector PvLEA-18.

AAC49859.1 U72764 Phaseolus vulgaris
putative osmoprotector. PvLEA-18. Pvlea-18. atypical late embryogenesis abundant protein.

AAF81194.1 AF240774 Phaseolus vulgaris
LEA-18.

SEQ ID NO: 672

CAB40743.1 AJ011885 Solanum tuberosum
starch branching enzyme II. sbe II.

CAB40746.1 AJ011888 Solanum tuberosum
starch branching enzyme II. SBE II.

CAB40748.1 AJ011890 Solanum tuberosum
starch branching enzyme II. SBE II.

AAD30186.1 AF076679 Triticum aestivum
starch branching enzyme-I. SBE-I.

AAD30187.1 AF076680 Aegilops tauschii
starch branching enzyme-I. SBE-I.

BAA82348.1 AB029548 Phaseolus vulgaris
branching enzyme I. kbeI.

CAA56319.1 X80009 Pisum sativum
starch branching enzyme I. SBEI.

CAB40747.1 AJ011889 Solanum tuberosum
starch branching enzyme II. SBE II.

CAA03846.1 AJ000004 Solanum tuberosum
branches 1,4- α glucans. starch branching enzyme II, SBE-II. Sbe-II.

BAA03738.1 D16201 Oryza sativa
branching enzyme-3 precursor.

AAG27623.1 AF286319 Triticum aestivum
starch branching enzyme 2. Sbe2. glucosyltransferase.

CAA72154.1 Y11282 Triticum aestivum
1,4- α -glucan branching enzyme II. sbe2.

AAK26821.1 AF338431 Aegilops tauschii
starch branching enzyme IIa. SBEIIa.

AAK26822.1 AF338432 Triticum aestivum
starch branching enzyme IIa variant. SBEIIa variant.

AAC33764.1 AF072725 Zea mays
starch branching enzyme IIb. ae. SBEIIb.

AAA18571.1 L08065 Zea mays
starch branching enzyme II.

BAA82828.1 AB023498 Oryza sativa
starch branching enzyme rbe4. RBE4.

AAC69753.1	AF064560	Hordeum vulgare	starch branching enzyme IIa. sbeIIa.
CAA56320.1	X80010	Pisum sativum	starch branching enzyme II. SBEII.
AAC69754.1	AF064561	Hordeum vulgare	starch branching enzyme IIb. sbeIIb.
AAC36471.1	AF072724	Zea mays	starch branching enzyme I. sbeI. confirmed by partial peptide sequencing.
AAA82735.1	U17897	Zea mays	starch branching enzyme I. sbeI.
AAD50279.2	AF169833	Sorghum bicolor	seed starch branching enzyme. SBE.
BAA01854.1	D11081	Zea mays	branching enzyme-I precursor.
CAA49463.1	X69805	Solanum tuberosum	1,4-alpha-glucan branching enzyme. SBE.
CAA70038.1	Y08786	Solanum tuberosum	1,4-alpha-glucan branching enzyme. sbeI.
AAB17086.1	U66376	Triticum aestivum	1,4-alpha-D-glucan 6-alpha-D-(1,4-alpha-D-glucanotransferase. branching enzyme.
AAB67316.1	U65948	Zea mays	formation of alpha-1-6 glucosidic linkage in starch biosynthesis. starch branching enzyme IIa. Sbe2a. starch branching enzyme isozyme SBEIIa.
BAB40334.1	AB042937	Ipomoea batatas	starch branching enzyme. IBE.
BAA01584.1	D10752	Oryza sativa	branching enzyme.
AAD28284.1	AF136268	Oryza sativa subsp. japonica	starch-branching enzyme I. RbeI.
BAA01616.1	D10838	Oryza sativa	1,4-alpha-glucan branching enzyme. sbeI.
BAA01855.1	D11082	Oryza sativa	branching enzyme-I precursor.
CAB40981.1	AJ237897	Triticum aestivum	starch branching enzyme I. sbeI. alternative.
CAB40979.1	AJ237897	Triticum aestivum	starch branching enzyme I. sbeI.
CAB40980.1	AJ237897	Triticum aestivum	starch branching enzyme I. sbeI. alternative.
AAG27622.1	AF286318	Triticum aestivum	starch branching enzyme 1. Sbe1A. glucosyltransferase.
CAA54308.1	X77012	Manihot esculenta	1,4-alpha-glucan branching enzyme. SBE.

CAA72987.1	Y12320	Triticum aestivum	starch branching enzyme I. Sbe1.
AAG27621.1	AF286317	Triticum aestivum	starch branching enzyme 1. Sbe1D. glucosyltransferase.
BAA82349.1	AB029549	Phaseolus vulgaris	branching enzyme 3. kbe3.
AAB61925.1	AF002820	Triticum aestivum	starch branching enzyme I. wSBE I-D2.
CAB40749.1	AJ011891	Solanum tuberosum	starch branching enzyme II. SBE II.
CAB40745.1	AJ011887	Solanum tuberosum	starch branching enzyme II. SBE II.
CAB40744.1	AJ011886	Solanum tuberosum	starch branching enzyme II. SBE II.
BAA85762.1	AB028067	Nicotiana tabacum	starch branching enzyme. SBE.
CAA49371.1	X69713	Manihot esculenta	branching enzyme. r-2.
BAB40335.1	AB042940	Ipomoea batatas	starch branching enzyme. IBE.
CAA49370.1	X69712	Manihot esculenta	branching enzyme. r-1.
AAC72336.1	AF064563	Hordeum vulgare	starch branching enzyme IIb. sbeIIb.
SEQ ID NO: 673			
CAA09881.1	AJ011939	Trifolium repens	peroxidase. prx2.
CAA62228.1	X90695	Medicago sativa	peroxidase2. prx2.
CAA71495.1	Y10469	Spinacia oleracea	peroxidase. prxr8.
AAB41812.1	L36158	Medicago sativa	peroxidase. pxdD. amino acid feature: conserved domains, aa 120 .. 126, 188 .. 195; amino acid feature: heme-binding domain, aa 63 .. 68.
BAA77387.1	AB024437	Scutellaria baicalensis	peroxidase 1.
AAF63024.1	AF244921	Spinacia oleracea	hydrogen peroxide catabolism. peroxidase prx12 precursor. type III peroxidase.
AAD11483.1	U51193	Glycine max	peroxidase. sEPb1.
AAB67737.1	L77080	Stylosanthes humilis	cationic peroxidase.

BAA07663.1	D42064	Nicotiana tabacum	cationic peroxidase isozyme 38K precursor.
BAA07664.1	D42065	Nicotiana tabacum	cationic peroxidase isozyme 40K precursor.
CAB94692.1	AJ242742	Ipomoea batatas	Removal of H ₂ O ₂ , oxidation of toxic reductants, defence response toward wounding. peroxidase. pod.
CAB67121.1	Y19023	Lycopersicon esculentum	peroxidase. cevi-1.
CAA62226.1	X90693	Medicago sativa	peroxidase1B. prx1B.
CAA50597.1	X71593	Lycopersicon esculentum	peroxidase. CEVI-1.
AAD11481.1	U51191	Glycine max	peroxidase precursor. sEPa1.
AAD11484.1	U51194	Glycine max	peroxidase. sEPb2.
BAA82306.1	AB027752	Nicotiana tabacum	peroxidase.
AAA65637.1	L13654	Lycopersicon esculentum	peroxidase. TPX1.
AAD11482.1	U51192	Glycine max	peroxidase precursor. sEPa2.
CAA62225.1	X90692	Medicago sativa	peroxidase1A. prx1A.
AAC98519.1	AF007211	Glycine max	peroxidase precursor. GMIPER1. pathogen-induced.
AAD37427.1	AF149277	Phaseolus vulgaris	peroxidase 1 precursor. FBP1. secretory peroxidase.
BAA14144.1	D90116	Armoracia rusticana	peroxidase isozyme.
AAA98491.1	L36981	Petroselinum crispum	anionic peroxidase.
CAA71488.1	Y10462	Spinacia oleracea	peroxidase. prxr1.
AAD43561.1	AF155124	Gossypium hirsutum	bacterial-induced peroxidase precursor. Perx_Goshiko.
BAA14143.1	D90115	Armoracia rusticana	peroxidase isozyme.
CAA71490.1	Y10464	Spinacia oleracea	peroxidase. prxr3.
AAB02554.1	L37790	Stylosanthes humilis	cationic peroxidase.

CAA66037.1	X97351	Populus balsamifera subsp. trichocarpa signal for ER. peroxidase.
BAA01877.1	D11102	Populus kitakamiensis peroxidase. prxA1.
CAA62227.1	X90694	Medicago sativa peroxidase1C. prx1C.
BAA07241.1	D38051	Populus kitakamiensis peroxidase. prxA4a.
BAA01950.1	D11337	Vigna angularis peroxidase.
AAF65464.2	AF247700	Oryza sativa peroxidase POC1.
AAF63027.1	AF244924	Spinacia oleracea hydrogen peroxide catabolism. peroxidase prx15 precursor. type III peroxidase.
CAC21393.1	AJ401276	Zea mays peroxidase. pox3.
CAA59487.1	X85230	Triticum aestivum peroxidase. pox4.
AAD37430.1	AF149280	Phaseolus vulgaris peroxidase 5 precursor. FBP5. secretory peroxidase.
CAA71491.1	Y10465	Spinacia oleracea peroxidase. prxr4.
AAB41811.1	L36157	Medicago sativa peroxidase. pxdC. amino acid feature: conserved domains, aa 123 .. 129, 191 .. 198; amino acid feature: heme-binding domain, aa 68 .. 73.
BAA03644.1	D14997	Oryza sativa peroxidase.
AAA32676.1	M37637	Arachis hypogaea cationic peroxidase. PNC2.
CAA71494.1	Y10468	Spinacia oleracea peroxidase. prxr7.
AAA34050.1	M74103	Nicotiana glauca anionic peroxidase.
CAA40796.1	X57564	Armoracia rusticana peroxidase. peroxidase precursor.
SEQ ID NO: 674		
AAG31438.1	AF241793	Perilla frutescens limonene synthase.
BAA08367.1	D49368	Perilla frutescens limonene cyclase.
BAA21629.1	AB005744	Perilla frutescens catalyzing the cyclization of geranyl pyrophosphate to 1-limonene. 1-limonene synthase. gPFLC. similar to perilla PFLC-1:DDBJ Acc#D49368.

AAG31437.1	AF241792	Perilla frutescens	limonene synthase.
AAK06663.1	AF317695	Perilla frutescens var. frutescens	limonene synthase.
AAG31435.1	AF241790	Perilla citriodora	limonene synthase.
AAF65545.1	AF233894	Perilla citriodora	limonene synthase.
AAD50304.1	AF175323	Mentha longifolia	limonene synthase. monoterpene synthase.
AAC37366.1	L13459	Mentha spicata	4S-limonene synthase.
AAG01140.1	AF282875	Schizonepeta tenuifolia	(+)-4R-limonene synthase.
AAC61260.1	AF061285	Capsicum annuum	sesquiterpene cyclase. UV induced.
AAG09949.1	AF171216	Lycopersicon esculentum	vetispiradiene synthase. LEVS2. sesquiterpene cyclase.
AAF74977.1	AF270425	Gossypium hirsutum	(E,E)-farnesyl diphosphate cyclase. (+)-delta-cadinene synthase. cdn2. sesquiterpene cyclase.
BAA82141.1	AB023816	Solanum tuberosum	vetispiradiene synthase. PVS4. potato sesquiterpene cyclase.
BAA82092.1	AB022598	Solanum tuberosum	vetispiradiene synthase. PVS1. potato sesquiterpene cyclase.
AAF21053.1	AF212433	Capsicum annuum	UV-induced sesquiterpene cyclase. SC2.
BAA82109.1	AB022720	Solanum tuberosum	vetispiradiene synthase. PVS3. potato sesquiterpene cyclase; PVS3.
BAA82108.1	AB022719	Solanum tuberosum	vetispiradiene synthase. PVS2. potato sesquiterpene cyclase; PVS2.
AAC12784.1	U88318	Gossypium hirsutum	(E,E)-farnesyl diphosphate cyclizing. (+)-delta-cadinene synthase. cdn1. sesquiterpene cyclase; delta-cadinene synthase.
AAG24640.2	AF304444	Artemisia annua	sesquiterpene cyclase.
AAK15641.1	AF326117	Capsicum annuum	sesquiterpene cyclase. PSC2.
CAC12731.1	AJ271792	Artemisia annua	putative sesquiterpene cyclase. cASC125.
SEQ ID NO: 675			
CAA50609.1	X71609	Nicotiana tabacum	ras-related GTP-binding protein.

CAA98166.1	Z73938	Lotus japonicus
GTP-binding protein. RAB5A. rab5A.		
CAC24477.1	AJ296336	Cichorium intybus x Cichorium endivia
GTP binding protein. chi3154.		
CAC24476.1	AJ296335	Cichorium intybus x Cichorium endivia
GTP binding protein. chi3152.		
CAB57220.1	AJ249866	Cichorium intybus x Cichorium endivia
GTP binding protein. gtp2.		
CAB57219.1	AJ249865	Cichorium intybus x Cichorium endivia
GTP binding protein. gtp1.		
CAC24475.1	AJ296334	Cichorium intybus x Cichorium endivia
GTP binding protein. chi3153.		
CAA46112.1	X64941	Nicotiana plumbaginifolia
small GTP binding protein.		
CAC24474.1	AJ296333	Cichorium intybus x Cichorium endivia
GTP binding protein. chi3151.		
CAC19792.1	AJ292320	Oryza sativa
small GTP-binding protein, RAB family. RAB5A protein. rab5A.		
AAD28731.1	AF112964	Triticum aestivum
small GTP-binding protein. Sgp.		
CAA98167.1	Z73939	Lotus japonicus
GTP-binding protein. RAB5B. rab5B.		
CAA06922.1	AJ006225	Mesembryanthemum crystallinum
small GTP-binding protein. rab5B.		
AAG42497.1	AF323991	Oryza sativa
small GTP-binding protein RAB5B. rab5B.		
BAA84717.1	AB032761	Oryza sativa
GTP-binding protein. rab5B.		
AAG24438.1	AF304518	Oryza sativa
small GTP-binding protein RAB5B. rab5B.		
CAB57221.1	AJ249867	Cichorium intybus x Cichorium endivia
GTP binding protein. bl.5.		
CAA98180.1	Z73952	Lotus japonicus
GTP-binding protein. RAB11D. rab11D.		
CAA98181.1	Z73953	Lotus japonicus
GTP-binding protein. RAB11E. rab11E.		
BAA02114.1	D12546	Pisum sativum
GTP-binding protein.		
BAA02113.1	D12545	Pisum sativum
GTP-binding protein.		
BAA02116.1	D12548	Pisum sativum
GTP-binding protein.		

BAA02112.1	D12544	Pisum sativum	GTP-binding protein.
BAA02118.1	D12550	Pisum sativum	GTP-binding protein.
CAA98159.1	Z73931	Lotus japonicus	GTP-binding protein. RAB1B. rab1B.
CAB65172.1	AJ245570	Lycopersicon esculentum	putative role in secretion of cell wall modifying enzymes. Rab11 GTPase. Rab11a.
CAA89049.1	Z49190	Beta vulgaris	GTP-binding. small G protein.
BAA02110.1	D12542	Pisum sativum	GTP-binding protein.
AAB97114.1	U58853	Glycine max	small GTP-binding protein. sral.
BAA02904.1	D13758	Oryza sativa	ras-related GTP binding protein. ss230.
CAA98178.1	Z73950	Lotus japonicus	GTP-binding protein. RAB11B. rab11B.
CAA98177.1	Z73949	Lotus japonicus	GTP-binding protein. RAB11A. rab11A.
AAK15703.1	AF327517	Oryza sativa	GTP-binding protein.
AAF65510.1	AF108883	Capsicum annuum	small GTP-binding protein.
BAA76422.1	AB024994	Cicer arietinum	rab-type small GTP-binding protein.
CAA98160.1	Z73932	Lotus japonicus	GTP-binding protein. RAB1C. rab1C.
AAA80680.1	U38466	Lycopersicon esculentum	small GTP-binding protein. LeRab1C. ; YPT1/Rab1A homolog LeRab1C.
AAA80678.1	U38464	Lycopersicon esculentum	small GTP-binding protein. LeRab1A. ; YPT1/Rab1A homolog LeRab1A.
SEQ ID NO: 676			
AAA80499.1	U20594	Lycopersicon esculentum	leucine aminopeptidase.
CAA54314.1	X77015	Solanum tuberosum	leucine aminopeptidase. LAP.
CAA48038.1	X67845	Solanum tuberosum	leucine aminopeptidase. LAP.
AAC49457.1	U50152	Lycopersicon esculentum	peptidase. leucine aminopeptidase. lap2.

AAC49456.1 U50151 *Lycopersicon esculentum*
exoprotease in the defense response. leucine aminopeptidase. lap.

AAA80498.1 U20593 *Lycopersicon esculentum*
leucine aminopeptidase.

CAA68143.1 X99825 *Petroselinum crispum*
cytosol aminopeptidase. leucine aminopeptidase.

BAA90521.1 AB037678 *Phaseolus vulgaris*
leucine aminopeptidase.

SEQ ID NO: 678

CAC09580.1 AJ298992 *Fagus sylvatica*
Absciscic acid (ABA) and calcium induced protein kinase. protein kinase (PK). pk1.

AAA34002.1 M67449 *Glycine max*
protein kinase. PK6.

AAK11734.1 AY027437 *Arachis hypogaea*
serine/threonine/tyrosine kinase.

BAB16918.1 AP002863 *Oryza sativa*
putative protein kinase. P0005A05.22.

CAA06334.1 AJ005077 *Lycopersicon esculentum*
protein kinase. TCTR2 protein. TCTR2.

AAG31141.1 AF305911 *Oryza sativa*
EDR1. EDR1. MAP kinase kinase kinase; similar to *Arabidopsis thaliana* EDR1.

CAA73722.1 Y13273 *Lycopersicon esculentum*
putative protein kinase.

AAD46406.1 AF096250 *Lycopersicon esculentum*
ethylene-responsive protein kinase TCTR1. ER50. serine/threonine kinase; similar to *Arabidopsis thaliana* negative regulator of the ethylene response pathway encoded by GenBank Accession Number L08789.

AAG31142.1 AF305912 *Hordeum vulgare*
EDR1. EDR1. MAP kinase kinase kinase; similar to *Arabidopsis thaliana* EDR1.

AAD10056.1 AF110518 *Lycopersicon esculentum*
ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit ripening inducible CTR1-like protein kinase; TCTR1.

AAD10057.1 AF110519 *Lycopersicon esculentum*
ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit ripening inducible CTR1-like protein kinase; TCTR1v.

AAK30005.1 AY029067 *Rosa hybrid cultivar*
CTR2 protein kinase.

BAB39409.1 AP002901 *Oryza sativa*
putative protein kinase. P0456F08.9. contains EST C23560(R0290).

BAA87853.1 AP000816 *Oryza sativa*
EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).

BAA06538.1	D31737	Nicotiana tabacum	protein-serine/threonine kinase.
BAB21240.1	AP002953	Oryza sativa	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
BAA94528.1	AP001800	Oryza sativa	Similar to Arabidopsis thaliana chromosome 2 BAC T20K24; putative receptor-like protein kinase (AC002392).
BAB17126.1	AP002867	Oryza sativa	putative receptor kinase. P0463F06.16.
BAB39451.1	AP003338	Oryza sativa	putative receptor kinase. OJ1212_B09.24.
BAB17348.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.32.
BAB17321.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.1.
BAB17129.1	AP002867	Oryza sativa	putative receptor kinase. P0463F06.20.
AAF68398.1	AF237568	Oryza sativa	receptor-like protein kinase. RLG2.
BAB07905.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.13.
BAA94517.1	AP001800	Oryza sativa	Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAB17335.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.17. contains ESTs D47575(S13157),AU032665(S13157).
BAB39441.1	AP003338	Oryza sativa	putative receptor kinase. OJ1212_B09.11.
BAB17116.1	AP002867	Oryza sativa	putative receptor kinase. P0463F06.3.
AAF78044.1	AF248493	Oryza sativa	receptor-like kinase. RLG18. protein kinase.
CAB51834.1	00069	Oryza sativa	l1332.5. contains eukaryotic protein kinase domain PF.
BAB17127.1	AP002867	Oryza sativa	putative receptor kinase. P0463F06.17.
AAF78021.1	AF238477	Oryza sativa	receptor-like kinase. RLG5. protein kinase.
AAD46420.1	AF100771	Hordeum vulgare	receptor-like kinase. Hv3ARK. similar to wheat ARK1AS.
AAD46917.1	AF164021	Oryza sativa	receptor kinase.
BAB17345.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.29.

BAB39438.1	AP003338	Oryza sativa	putative receptor kinase. OJ1212_B09.7.
AAF78018.1	AF238474	Oryza sativa	receptor-like kinase. RLG16. protein kinase.
AAC01746.1	AF044489	Oryza sativa	receptor-like protein kinase. drpk1.
BAB17337.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.21. contains ESTs D47575(S13157),AU032665(S13157).
BAB17347.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.31. contains ESTs D47575(S13157),AU032665(S13157).
BAB17344.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.28. contains ESTs D47575(S13157),AU032665(S13157).
BAB39437.1	AP003338	Oryza sativa	receptor-like kinase. OJ1212_B09.6.
AAF78019.1	AF238475	Oryza sativa	receptor-like kinase. RLG17. protein kinase.
BAA05648.1	D26601	Nicotiana tabacum	protein kinase.
BAB17332.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.13. contains ESTs D47575(S13157),AU032665(S13157).
BAB39435.1	AP003338	Oryza sativa	putative receptor kinase. OJ1212_B09.2.
SEQ ID NO: 679			
CAA78386.1	Z13996	Petunia x hybrida	DNA binding protein; transcriptional activator. protein 1. myb.Ph3. Product related to animal myb proto-oncoproteins. Sequence from nucleotide 992 is not included in clone cPF1 and has been obtained by PCR amplification of cDNA.
CAB43399.1	AJ006292	Antirrhinum majus	Myb-related transcription factor mixta-like 1. mybm11.
CAA67600.1	X99210	Lycopersicon esculentum	myb-related transcription factor. THM16.
BAA23337.1	D88617	Oryza sativa	transfactor. OSMYB1. Osmyb1.
AAA82943.1	U39448	Picea mariana	MYB-like transcriptional factor MBF1. putative DNA binding region highly similar to the maize C1.
CAA64614.1	X95296	Lycopersicon esculentum	transcription factor. THM27. myb-related.
BAA93038.1	AP001552	Oryza sativa	EST AU082058(C12976) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana putative transcription factor (AF062916).

AAC04720.1	AF034134	Gossypium hirsutum	putative MYB-like transcription factor. MYB-like DNA-binding domain protein. Cmy-O. similar to MYB A encoded by GenBank Accession Number L04497.
CAA72186.1	Y11351	Oryza sativa	myb factor. myb.
AAF22256.1	AF161711	Pimpinella brachycarpa	myb-related transcription factor.
BAB39987.1	AP003020	Oryza sativa	putative transcription factor (myb). P0498A12.16. contains ESTs AU097474(S5087),D40175(S1959).
BAB39972.1	AP003018	Oryza sativa	putative transcription factor (myb). OSJNBa0004B13.27. contains ESTs AU097474(S5087),D40175(S1959).
BAA23338.1	D88618	Oryza sativa	transfactor. OSMYB2. Osmyb2.
BAA88222.1	AB028650	Nicotiana tabacum	myb-related transcription factor LBM2. lbm2.
CAA67575.1	X99134	Lycopersicon esculentum	transcription factor. THM6. myb-related.
CAA78387.1	Z13997	Petunia x hybrida	DNA-binding protein, transcriptional activator. protein 2. myb.Ph2. related to animal myb proto-oncoproteins.
CAA66952.1	X98308	Lycopersicon esculentum	THM18. myb-related transcription factor.
BAA23339.1	D88619	Oryza sativa	transfactor. OSMYB3. Osmyb3.
AAC49394.1	U57002	Zea mays	P protein. P. allele P-wr; Myb-like transcriptional regulator with a putative zinc-finger at the C-terminal.
AAB41101.1	U72762	Nicotiana tabacum	transcription factor Myb1. myb1. TMV-inducible Myb homolog; contains helix-turn-helix motif; contains redox-sensitive cysteine.
AAA33500.1	M73028	Zea mays	myb-like transcription factor. P.
AAG36774.1	AF210616	Zea mays	P2 protein. P2. myb-like transcriptional factor; similar to Zea mays P gene.
BAA88223.1	AB028651	Nicotiana tabacum	myb-related transcription factor LBM3. lbm3.
BAA88224.1	AB028652	Nicotiana tabacum	myb-related transcription factor LBM4. lbm4.
CAA72187.1	Y11352	Oryza sativa	myb factor. myb.

BAA88221.1	AB028649	Nicotiana tabacum	myb-related transcription factor LBM1. lbm1.
CAA72185.1	Y11350	Oryza sativa	myb factor. myb.
AAG13574.1	AC037425	Oryza sativa	myb factor. OSJNBa0055P24.4.
SEQ ID NO: 680			
AAA34238.1	L20507	Vigna radiata	calmodulin.
AAA34014.1	L01432	Glycine max	calcium-binding regulatory protein. calmodulin. SCaM-3. putative.
AAA34013.1	L01430	Glycine max	calcium-binding regulatory protein. calmodulin. SCaM-1. putative.
CAA36644.1	X52398	Medicago sativa	calmodulin (AA 1-149).
AAD10245.1	AF030033	Phaseolus vulgaris	calmodulin. CaM. EF-hand protein; calcium-dependent protein; functions in calcium signal transduction pathways.
AAD10244.1	AF030032	Phaseolus vulgaris	calmodulin. CaM. EF-hand protein; calcium-dependent protein; functions in calcium signal transduction pathways.
CAA74307.1	Y13974	Zea mays	calmodulin.
CAA46150.1	X65016	Oryza sativa	calmodulin. cam.
AAC36058.1	AF042839	Oryza sativa	calmodulin. CaM2.
AAD10246.1	AF030034	Phaseolus vulgaris	calmodulin. CaM. EF-hand protein; calcium-dependent protein; functions in calcium signal transduction pathways.
CAA54583.1	X77397	Zea mays	calmodulin. CaM2.
BAA87825.1	AP000815	Oryza sativa	ESTs AU030013(E50493),AU081341(E50493) correspond to a region of the predicted gene. Similar to O.sativa gene encoding calmodulin. (Z12828).
AAA92681.1	U13882	Pisum sativum	calcium-binding protein. calmodulin.
AAA33706.1	M80836	Petunia x hybrida	calmodulin. CAM81.
AAA33705.1	M80831	Petunia x hybrida	calmodulin-related protein. CAM53.
CAA43143.1	X60738	Malus x domestica	Calmodulin. CaM.

CAA78301.1	Z12839	<i>Lilium longiflorum</i> calcium binding protein, signal transduction. calmodulin.
AAA33397.1	L18912	<i>Lilium longiflorum</i> calcium binding protein, signal transduction. calmodulin. putative.
CAA42423.1	X59751	<i>Daucus carota</i> calmodulin. Ccam-1.
CAA67054.1	X98404	<i>Capsicum annuum</i> calmodulin-2.
AAG27432.1	AF295637	<i>Elaeis guineensis</i> calmodulin.
AAG11418.1	AF292108	<i>Prunus avium</i> calmodulin.
AAA34237.1	L20691	<i>Vigna radiata</i> calmodulin.
AAC49587.1	U49105	<i>Triticum aestivum</i> calmodulin TaCaM4-1. calcium-binding protein.
AAC49586.1	U49104	<i>Triticum aestivum</i> calmodulin TaCaM3-3. calcium-binding protein.
AAC49585.1	U49103	<i>Triticum aestivum</i> calmodulin TaCaM3-2. calcium-binding protein.
AAC49584.1	U48693	<i>Triticum aestivum</i> calmodulin TaCaM3-1. calcium-binding protein.
AAC49583.1	U48692	<i>Triticum aestivum</i> calmodulin TaCaM2-3. calcium-binding protein.
AAC49582.1	U48691	<i>Triticum aestivum</i> calmodulin TaCaM2-2. calcium-binding protein.
AAC49580.1	U48689	<i>Triticum aestivum</i> calmodulin TaCaM1-3. calcium-binding protein.
AAC49579.1	U48688	<i>Triticum aestivum</i> calmodulin TaCaM1-2. calcium binding protein.
AAC49578.1	U48242	<i>Triticum aestivum</i> calmodulin TaCaM1-1. calcium-binding.
AAA03580.1	L01431	<i>Glycine max</i> calcium-binding regulatory protein. calmodulin. SCaM-2. putative.
AAB36130.1	S81594	<i>Vigna radiata</i> auxin-regulated calmodulin. auxin-regulated calmodulin, arCaM. This sequence comes from Fig. 1; arCaM.
AAA33901.1	L18913	<i>Oryza sativa</i> calcium binding protein, signal transduction. calmodulin. putative.
CAA78287.1	Z12827	<i>Oryza sativa</i> calcium binding protein, signal transduction. calmodulin.
AAB46588.1	U83402	<i>Capsicum annuum</i> calmodulin.

CAA61980.1	X89890	Bidens pilosa	Calmodulin.
AAA32938.1	M27303	Hordeum vulgare	calmodulin.
BAA88540.1	AP000969	Oryza sativa	ESTs AU081349(E61253), D41425(S3918) correspond to a region of the predicted gene. Similar to calmodulin. (AF042840).
AAF65511.1	AF108889	Capsicum annuum	calmodulin.
AAC36059.1	AF042840	Oryza sativa	calmodulin. CaM1.
AAA33900.1	L18914	Oryza sativa	calcium binding protein, signal transduction. calmodulin.
CAA78288.1	Z12828	Oryza sativa	calcium binding protein, signal transduction. calmodulin.
AAA34015.1	L01433	Glycine max	calcium-binding regulatory protein. calmodulin. SCaM-4. putative.
AAA16320.1	L14071	Bryonia dioica	calmodulin. Bc329. calcium-binding sites (amino acid #): 1. (21..33); 2. (57..68); 3. (94..106); 4. (130..141).
AAA19571.1	U10150	Brassica napus	calcium binding. calmodulin. bcm1.
AAA87347.1	M88307	Brassica juncea	calmodulin.
CAA52602.1	X74490	Zea mays	Calmodulin. ZMCALM1.
SEQ ID NO: 683			
CAA71800.1	Y10847	Brassica juncea	O-acetylserine(thiol) lyase.
CAA71798.1	Y10845	Brassica juncea	O-acetylserine(thiol) lyase.
AAC25635.1	AF044172	Solanum tuberosum	cysteine synthase. CS-A; O-acetylserine (thiol) lyase; cytosolic isoform.
BAA01279.1	D10476	Spinacia oleracea	O-acetylserine(thiol) lyase.
BAA02438.1	D13153	Triticum aestivum	O-acetylserine (thiol) lyase. cys1.
CAA59798.1	X85803	Zea mays	O-acetylserine (thiol) lyase. Mcysp. cysteine synthase.
AAD23907.1	AF073695	Oryza sativa	cysteine synthase. rcs1. O-acetylserine(thiol)-lyase.
AAD23909.1	AF073697	Oryza sativa	cysteine synthase. rcs3. O-acetylserine(thiol)-lyase.

AAC25636.1	AF044173	Solanum tuberosum	cysteine synthase. CS-B; O-acetylserine (thiol) lyase; plastidic isoform.
AAC27794.1	AF078693	Chlamydomonas reinhardtii	cysteine biosynthesis. putative O-acetylserine(thiol)lyase precursor. Crcys-1A.
CAA06819.1	AJ006024	Cicer arietinum	cysteine synthase, O-acetyl-L-serine (thiol)-lyase.
CAA46086.1	X64874	Capsicum annuum	O-acetylserine (thiol)-lyase.
CAA71799.1	Y10846	Brassica juncea	O-acetylserine(thiol) lyase.
AAA16973.1	L05184	Chloroplast Spinacia oleracea	O-acetylserine-(thiol)-lyase.
AAD23908.1	AF073696	Oryza sativa	cysteine synthase. rcs2. O-acetylserine(thiol)-lyase.
AAD23910.1	AF073698	Oryza sativa	cysteine synthase. rcs4. O-acetylserine(thiol)-lyase.
SEQ ID NO: 684			
AAA68983.1	L12395	Brassica napus	signal transduction, membrane vehicle traffic. small GTP-binding protein. bra. putative.
SEQ ID NO: 685			
AAB61961.1	L81152	Oryza sativa	integral membrane protein. OsNramp2.
AAB36424.1	S81897	Oryza sativa	OsNramp1. OsNramp1. Nramp1 homolog/Bcg product homolog; This sequence comes from Fig. 2.
AAB62273.1	L41217	Oryza sativa	integral membrane protein. OsNramp1. putative.
AAC49720.1	U60767	Oryza sativa	integral membrane protein OsNramp3. OsNramp3.
SEQ ID NO: 686			
AAC04719.1	AF034133	Gossypium hirsutum	putative MYB-like transcription factor. MYB-like DNA-binding domain protein. CmY-N. similar to MYB A encoded by GenBank Accession Number L04497.
AAB58314.1	U33917	Cratogeomys plantagineum	Cpm7. cpm7. putative DNA-binding protein; myb-like gene; myb-related transcription factor.
AAB58313.1	U33916	Cratogeomys plantagineum	Cpm5. cpm5. putative DNA-binding protein; myb-related gene; myb-related transcription factor.
AAC13876.1	U33915	Cratogeomys plantagineum	myb-related transcription factor Cpm10. cpm10. putative DNA-binding protein.

AAK08983.1	AY026332	Oryza sativa	Myb transcription factor JAMyb. related to host cell death and defense responses; induced by jasmonic acid, wounding, or infection of rice blast fungus, but not by salicylic acid or abscisic acid.
BAB18296.1	AP002860	Oryza sativa	putative myb-related transcription factor. P0409B08.23.
CAA71992.1	Y11105	Pisum sativum	Myb26.
BAB40790.1	AB058642	Lilium hybrid division I	LhMyb.
AAK19618.1	AF336285	Gossypium hirsutum	GHMYB38. ghmyb38. similar to myb.
CAA78387.1	Z13997	Petunia x hybrida	DNA-binding protein, transcriptional activator. protein 2. myb.Ph2. related to animal myb proto-oncoproteins.
BAA88221.1	AB028649	Nicotiana tabacum	myb-related transcription factor LBM1. lbm1.
BAA88224.1	AB028652	Nicotiana tabacum	myb-related transcription factor LBM4. lbm4.
AAK19617.1	AF336284	Gossypium hirsutum	GHMYB36. ghmyb36. similar to myb.
AAA33067.1	L04497	Gossypium hirsutum	MYB A; putative.
AAK19615.1	AF336282	Gossypium hirsutum	GHMYB10. ghmyb10. similar to myb.
BAA81733.2	AB029162	Glycine max	GmMYB29A2.
BAA81732.1	AB029161	Glycine max	GmMYB29A2.
BAA81730.1	AB029159	Glycine max	GmMYB29A1.
BAA88223.1	AB028651	Nicotiana tabacum	myb-related transcription factor LBM3. lbm3.
AAB41101.1	U72762	Nicotiana tabacum	transcription factor Myb1. myb1. TMV-inducible Myb homolog; contains helix-turn-helix motif; contains redox-sensitive cysteine.
BAA81736.1	AB029165	Glycine max	GmMYB29B2.
BAA81731.1	AB029160	Glycine max	GmMYB29A1.
CAA72218.1	Y11415	Oryza sativa	myb.

CAA67000.1	X98355	Oryza sativa	activator of alpha-amylase gene promoter. transcription factor GAMyb. Gam1. Myb-like; expression is regulated by gibberellin.
AAK19611.1	AF336278	Gossypium hirsutum	BNLGH1233. bnlghi6233. similar to myb.
CAA67575.1	X99134	Lycopersicon esculentum	transcription factor. THM6. myb-related.
CAA64614.1	X95296	Lycopersicon esculentum	transcription factor. THM27. myb-related.
AAD31395.1	AF114162	Lolium temulentum	gibberellin MYB transcription factor. GAMyb. R2/R3-MYB.
BAA93038.1	AP001552	Oryza sativa	EST AU082058(C12976) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana putative transcription factor (AF062916).
AAG22863.1	AY008692	Hordeum vulgare	transcription factor GAMyb. Gamyb.
BAA96421.1	AB044084	Triticum aestivum	transcription activator for gibberellin response. GAMyb protein. Ta-GAMyb.
CAA61021.1	X87690	Hordeum vulgare	transcriptional activator of alpha-amylase gene promoter. GAMyb protein. Gam1.
CAA66952.1	X98308	Lycopersicon esculentum	THM18. myb-related transcription factor.
AAC49394.1	U57002	Zea mays	P protein. P. allele P-wr; Myb-like transcriptional regulator with a putative zinc-finger at the C-terminal.
BAA88222.1	AB028650	Nicotiana tabacum	myb-related transcription factor LBM2. lbm2.
AAG36774.1	AF210616	Zea mays	P2 protein. P2. myb-like transcriptional factor; similar to Zea mays P gene.
AAA33500.1	M73028	Zea mays	myb-like transcription factor. P.
CAC19439.1	AJ237661	Oryza sativa	Myb factor protein. myb.
CAB40189.1	AJ133638	Avena sativa	transcriptional activator. myb protein. gamyb.
AAK19619.1	AF336286	Gossypium hirsutum	GHMYB9. ghmyb9. similar to myb.
AAC04720.1	AF034134	Gossypium hirsutum	putative MYB-like transcription factor. MYB-like DNA-binding domain protein. CmY-O. similar to MYB A encoded by GenBank Accession Number L04497.
AAC04716.1	AF034130	Gossypium hirsutum	putative MYB-like transcription factor. MYB-like DNA-binding domain protein. CmY-D. similar to MYB A encoded by GenBank Accession Number L04497.

AAG28526.1	AF198499	Nicotiana tabacum	anther-specific myb-related protein 1. mybAS1. NtMYBAS1; contains N-terminal R2, R3 myb domain repeats similar to c-myb.
CAA78388.1	Z13998	Petunia x hybrida	DNA-binding protein; transcriptional activator. protein 3. myb.Ph3. related to animal myb proto-oncoproteins.
AAA33482.1	M37153	Zea mays	c1 locus myb homologue; putative.
AAK09327.1	AF320614	Zea mays	activates anthocyanin transcription. anthocyanin regulatory C1. c1. transcription factor.
AAK09326.1	AF320613	Zea mays	activates anthocyanin transcription. anthocyanin regulatory C1. c1. transcription factor.
SEQ ID NO: 687			
BAA92972.1	AP001551	Oryza sativa	ESTs AU056183(S20356),AU056881(S20950) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 4 BAC clone F6I18 ; putative protein kinase. (AL022198).
BAA83689.1	AB011968	Oryza sativa	OsPK7. OsPK7. protein kinase.
BAA83688.1	AB011967	Oryza sativa	OsPK4. OsPK4. protein kinase.
AAF22219.1	AF141378	Zea mays	protein kinase PK4. ZmPK4.
BAA34675.1	AB011670	Triticum aestivum	wpk4 protein kinase. wpk4.
CAA73068.1	Y12465	Sorghum bicolor	serine/threonine kinase. SNFL2.
CAA73067.1	Y12464	Sorghum bicolor	serine/threonine kinase. SNFL1.
BAA92970.1	AP001551	Oryza sativa	Similar to Arabidopsis thaliana chromosome 4 BAC clone F28A21 ; putative protein kinase. (AL035526).
CAA74646.1	Y14274	Sorghum bicolor	putative serine/threonine protein kinase. SNFL3.
AAD31900.1	AF145482	Mesembryanthemum crystallinum	putative serine/threonine protein kinase.
AAB62693.1	AF004947	Oryza sativa	protein kinase.
BAA96628.1	AP002482	Oryza sativa	ESTs D41739(S4522),AU055999(S20214), AU057588(S21592 correspond to a region of the predicted gene. Similar to Sorghum bicolor serine/threonine kinase (Y12465).

AAD23582.1	AF128443	Glycine max	probably involved in plant stress responses possibly regulates gene expression. SNF-1-like serine/threonine protein kinase. expressed in nodules, roots and leaves.
BAA05649.1	D26602	Nicotiana tabacum	protein kinase.
CAA71142.1	Y10036	Cucumis sativus	SNF1-related protein kinase.
AAC99329.1	AF062479	Oryza sativa	protein kinase SNF1. Snf1. similar to yeast SNF1.
CAA65244.1	X95997	Solanum tuberosum	SNF1-related protein kinase. PKIN1.
CAA57898.1	X82548	Hordeum vulgare	SNF1-related protein kinase. BKIN2.
CAA07813.1	AJ007990	Hordeum vulgare	SnRK1-type protein kinase. kin12a.
CAA46556.1	X65606	Hordeum vulgare	protein kinase. BKIN12.
AAB05457.1	U55768	Oryza sativa	SNF1-related protein kinase. RSk1. Ser/Thr protein kinase homolog.
CAA46554.1	X65604	Hordeum vulgare	protein kinase. BKIN12.
AAD00239.1	U73938	Nicotiana tabacum	protein kinase. PK11-C1. PK11-C1. induced at the transcriptional level by the abscisic acid plant hormone; similar to serine/threonine protein kinase.
AAC69450.1	AF032465	Nicotiana tabacum	putative serine/threonine protein kinase. WAPK.
AAD00240.1	U73939	Nicotiana tabacum	protein kinase. PK11-C5. PK11-C5. induced at the transcriptional level by the abscisic acid plant hormone; similar to serine/threonine protein kinase.
BAA13608.1	D88399	Oryza sativa	serine-threonine kinase. endosperm kinase. REK.
AAA34017.1	L19360	Glycine max	protein kinase 2. SPK-2. putative.
AAG60195.1	AC084763	Oryza sativa	protein kinase REK. OSJNBa0027P10.6.
AAA33004.1	L12394	Brassica napus	serine/threonine protein kination. serine/threonine protein kinase. BSK2. putative.
BAA19573.1	AB002109	Oryza sativa	protein kinase. a novel protein kinase.
AAA33979.1	L01453	Glycine max	protein phosphorylation, regulatory protein. protein kinase. SPK-1. putative.
AAA33003.1	L12393	Brassica napus	protein kination. serine/threonine protein kinase. BSK1. putative.

AAB68962.1 L38855 Glycine max
protein kinase. SPK-4.

AAB68961.1 L19361 Glycine max
protein kinase 3. SPK-3. putative.

AAB58348.1 U29095 Triticum aestivum
serine-threonine protein kinase. TaPK3.

AAF27340.1 AF186020 Vicia faba
abscisic acid-activated protein kinase. AAPK.

AAA96325.1 M94726 Triticum aestivum
protein kinase. abscisic acid inducible.

CAA81443.1 Z26846 Mesembryanthemum crystallinum
protein kinase. MCPK9.

AAG31326.1 AF178575 Vitis vinifera
putative serine/threonine kinase GDBrPK. GDBrPK. similar to SNF protein kinase.

CAA06503.1 AJ005373 Craterostigma plantagineum
protein kinase. cppk1.

AAF21062.1 AF216527 Dunaliella tertiolecta
calcium-dependent protein kinase. CPK1; CDPK.

CAA89202.1 Z49233 Chlamydomonas eugametos
calcium-stimulated protein kinase.

SEQ ID NO: 689

AAC49826.1 U71604 Catharanthus roseus
involved in the second to last step in vindoline biosynthesis. desacetoxyvindoline 4-
hydroxylase. CRSD4H. 2-oxoglutarate dependent dioxygenase.

AAB97311.1 AF008597 Catharanthus roseus
desacetoxyvindoline-4-hydroxylase. CRSD4H. 2-oxoglutarate dependent dioxygenase;
involved in the second to last step in vindoline biosynthesis.

AAC49827.1 U71605 Catharanthus roseus
involved in the second to last step in vindoline biosynthesis. desacetoxyvindoline 4-
hydroxylase. CRSD4H. 2-oxoglutarate dependent dioxygenase.

BAA37127.1 AB012203 Lactuca sativa
2-oxoglutarate-dependent dioxygenase. gibberelin 20-oxidase. Ls20ox1.

BAA95828.1 AP002069 Oryza sativa
ESTs D47168(S12332),D46350(S10967) correspond to a region of the predicted gene.
Similar to Prunus armeniaca ethylene-forming-enzyme-like dioxygenase. (U97530).

AAD56580.1 AF184273 Daucus carota
leucoanthocyanidin dioxygenase 1. LDOX1. 2-oxoglutarate dependent dioxygenase.

AAB39995.1 U82432 Dianthus caryophyllus
anthocyanidin synthase. allele: S; 2-oxoglutarat-dependent dioxygenase.

AAD56581.1 AF184274 Daucus carota
leucoanthocyanidin dioxygenase 2. LDOX. 2-oxoglutarate dependent dioxygenase.

SEQ ID NO: 691

AAA34002.1	M67449	Glycine max protein kinase. PK6.
CAC09580.1	AJ298992	Fagus sylvatica Absciscic acid (ABA) and calcium induced protein kinase. protein kinase (PK). pk1.
AAK11734.1	AY027437	Arachis hypogaea serine/threonine/tyrosine kinase.
BAB16918.1	AP002863	Oryza sativa putative protein kinase. P0005A05.22.
CAA06334.1	AJ005077	Lycopersicon esculentum protein kinase. TCTR2 protein. TCTR2.
AAD10057.1	AF110519	Lycopersicon esculentum ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit ripening inducible CTR1-like protein kinase; TCTR1v.
AAD10056.1	AF110518	Lycopersicon esculentum ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit ripening inducible CTR1-like protein kinase; TCTR1.
CAA73722.1	Y13273	Lycopersicon esculentum putative protein kinase.
AAD46406.1	AF096250	Lycopersicon esculentum ethylene-responsive protein kinase TCTR1. ER50. serine/threonine kinase; similar to Arabidopsis thaliana negative regulator of the ethylene response pathway encoded by GenBank Accession Number L08789.
AAG31141.1	AF305911	Oryza sativa EDR1. EDR1. MAP kinase kinase kinase; similar to Arabidopsis thaliana EDR1.
AAG31142.1	AF305912	Hordeum vulgare EDR1. EDR1. MAP kinase kinase kinase; similar to Arabidopsis thaliana EDR1.
AAK30005.1	AY029067	Rosa hybrid cultivar CTR2 protein kinase.
AAK21965.1	AY028699	Brassica napus receptor protein kinase PERK1.
BAB16871.1	AP002537	Oryza sativa putative protein kinase APK1A Arabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192), D25110(R3192).
AAF91323.1	AF244889	Glycine max receptor-like protein kinase 2. RLK2. GmRLK2.
AAF91324.1	AF244890	Glycine max receptor-like protein kinase 3. RLK3. GmRLK3.
AAK00425.1	AC069324	Oryza sativa Putative protein kinase. OSJNBa0071K19.11.
BAB39409.1	AP002901	Oryza sativa putative protein kinase. P0456F08.9. contains EST C23560(R0290).
AAF91322.1	AF244888	Glycine max receptor-like protein kinase 1. RLK1. GmRLK1.

BAB18292.1	AP002860	Oryza sativa	putative receptor-like protein kinase. P0409B08.19.
AAK16409.1	AF320086	Zea mays	serine threonine kinase 1. stk1. expressed in mature tassel.
BAA06538.1	D31737	Nicotiana tabacum	protein-serine/threonine kinase.
BAA21132.1	D88193	Brassica rapa	S-receptor kinase. SRK9 (B.c).
BAA06285.1	D30049	Brassica rapa	S-receptor kinase SRK9.
BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
CAB54520.1	AJ238845	Brassica napus	putative role in cell cycle control. MAP3K epsilon 1 protein kinase. MAP3Kel.
CAA97692.1	Z73295	Catharanthus roseus	receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
CAA08995.1	AJ010091	Brassica napus	MAP3K alpha 1 protein kinase. MAP3K alpha 1.
BAB40094.1	AP003210	Oryza sativa	putative receptor protein kinase. OSJNBa0010K01.7.
CAB51834.1	00069	Oryza sativa	11332.5. contains eukaryotic protein kinase domain PF.
BAB40021.1	AP003021	Oryza sativa	putative wall-associated kinase 2. P0503E05.25. contains EST C24950(S16264).
AAF43496.1	AF131222	Lophopyrum elongatum	protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.
AAK11674.1	AF339747	Lophopyrum elongatum	protein kinase. ESI47.
AAA62232.1	U00443	Brassica napus	S-receptor kinase. protein contains an immunoglobulin-like domain.
BAB40010.1	AP003021	Oryza sativa	putative wall-associated kinase 2. P0503E05.12.
AAC36318.1	AF053127	Malus x domestica	leucine-rich receptor-like protein kinase. LRPKm1.
AAC23542.1	U20948	Ipomoea trifida	receptor protein kinase. IRK1.
BAA23676.1	AB000970	Brassica rapa	receptor kinase 1. BcRK1.
BAB18321.1	AP002865	Oryza sativa	putative receptor protein kinase. P0034C11.11.

BAA92836.1	AB032473	Brassica oleracea	S18 S-locus receptor kinase. SRK18.
AAA33915.1	L27821	Oryza sativa	receptor type serine/threonine kinase. protein kinase.
BAB40081.1	AP003074	Oryza sativa	putative receptor protein kinase. OSJNBa0004G10.30.
AAD38286.1	AC007789	Oryza sativa	putative protein kinase. OSJNBa0049B20.13.
BAA92837.1	AB032474	Brassica oleracea	S60 S-locus receptor kinase. SRK60.
SEQ ID NO: 692			
AAK16172.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.14.
AAF17077.1	AF199453	Sorghum bicolor	UDP-glucose glucosyltransferase. UDP-glucose:p-hydroxymandelonitrile-o-glucosyltransferase.
AAF61647.1	AF190634	Nicotiana tabacum	UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.
BAA89009.1	AB027455	Petunia x hybrida	anthocyanin 5-O-glucosyltransferase. PH1.
AAF98390.1	AF287143	Brassica napus	catalyzes the transfer of glucose from UDP-glucose to sinapate and some other hydroxycinnamates (4-coumarate, caffeate, ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.
AAD21086.1	AF127218	Forsythia x intermedia	adds glucose residue to position 3 of flavonoid compounds. flavonoid 3-O-glucosyltransferase. UFGT.
BAA93039.1	AB033758	Citrus unshiu	limonoid UDP-glucosyltransferase. LGTase.
BAA83484.1	AB031274	Scutellaria baicalensis	UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.
BAA12737.1	D85186	Gentiana triflora	UDP-glucose:flavonoid-3-glucosyltransferase.
CAA54612.1	X77462	Manihot esculenta	UTP-glucose glucosyltransferase. CGT5.
BAA19155.1	AB000623	Nicotiana tabacum	glucosyl transferase. JIGT.
BAA89008.1	AB027454	Petunia x hybrida	anthocyanidin 3-O-glucosyltransferase. PGT8.
BAB17060.1	AP002523	Oryza sativa	putative glucosyl transferase. P0013F10.6.
BAA90787.1	AB038248	Ipomoea batatas	UDP glucose: flavonoid 3-O-glucosyltransferase. uf3gt.

AAK16178.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.5.
AAK16175.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.15.
AAB36653.1	U32644	Nicotiana tabacum	immediate-early salicylate-induced glucosyltransferase. IS5a.
AAB36652.1	U32643	Nicotiana tabacum	immediate-early salicylate-induced glucosyltransferase. IS10a.
AAK28303.1	AF346431	Nicotiana tabacum	phenylpropanoid:glucosyltransferase 1. togt1. glucosyltransferase.
AAK28304.1	AF346432	Nicotiana tabacum	phenylpropanoid:glucosyltransferase 2. togt2. glucosyltransferase.
BAB17061.1	AP002523	Oryza sativa	putative glucosyl transferase. P0013F10.7. contains EST C73149(E2992).
CAA30761.1	X07940	Zea mays	UDPglucose flavonoid glycosyl-transferase. Bz-McC.
AAK16410.1	AF320086	Zea mays	UDPG-flavonoid 3-O-glucosyl transferase. bz.
CAA31855.1	X13500	Zea mays	UDPglucose:flavonol 3-O-glucosyltransferase.
BAB17059.1	AP002523	Oryza sativa	putative glucosyl transferase. P0013F10.5.
BAA36421.1	AB013596	Perilla frutescens	UDP-glucose:anthocynin 5-O-glucosyltransferase. PF3R4.
AAB86473.1	AF028237	Ipomoea purpurea	UDP glucose: flavonoid 3-O-glucosyltransferase. UF3GT-FL1.
CAA30760.1	X07937	Zea mays	UDPglucose flavonoid glycosyl transferase. Bz-W22.
BAB41021.1	AB047094	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT1.
BAB41019.1	AB047092	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT1.
BAB41025.1	AB047098	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT1.
AAD55985.1	AF165148	Petunia x hybrida	catalyzes the penultimate step of flavonol glucosylgalactoside biosynthesis from UDP-galactose and flavonol aglycones in petunia pollen. UDP-galactose:flavonol 3-O-galactosyltransferase. F3galtase.
BAB41018.1	AB047091	Vitis labrusca x Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT2. The gene originated in one of the parents V. vinifera cv. Centennial.

BAB41017.1 AB047090 *Vitis labrusca* x *Vitis vinifera*
 UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT1. The gene was derived from one of the parents *V. labruscana* cv. Ishiharawase.

AAK16181.1 AC079887 *Oryza sativa*
 putative glucosyltransferase. OSJNBa0040E01.16.

BAB41023.1 AB047096 *Vitis vinifera*
 UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT1.

CAA59450.1 X85138 *Lycopersicon esculentum*
 twil. homologous to glucosyltransferases.

CAA54614.1 X77464 *Manihot esculenta*
 UTP-glucose glucosyltransferase. CGT7.

AAB81682.1 AF000371 *Vitis vinifera*
 UDP glucose:flavonoid 3-o-glucosyltransferase.

AAB81683.1 AF000372 *Vitis vinifera*
 UDP glucose:flavonoid 3-o-glucosyltransferase.

BAB41024.1 AB047097 *Vitis vinifera*
 UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT2.

CAA54558.1 X77369 *Solanum melongena*
 glycosyl transferase. GT.

BAB41026.1 AB047099 *Vitis vinifera*
 UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT2.

BAB41020.1 AB047093 *Vitis vinifera*
 UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT2.

BAB41022.1 AB047095 *Vitis vinifera*
 UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT2.

BAA19659.1 AB002818 *Perilla frutescens*
 flavonoid 3-O-glucosyltransferase. UDP glucose.

AAG25643.1 AF303396 *Phaseolus vulgaris*
 UDP-glucosyltransferase HRA25. putative; defense associated.

SEQ ID NO: 694

BAB40923.1 AB059401 *Oryza sativa*
 putative selenium binding protein. Os SBP.

SEQ ID NO: 695

AAD26942.1 AF119050 *Datisca glomerata*
 zinc-finger protein 1. zfp1. DgZFP1.

BAA05079.1 D26086 *Petunia x hybrida*
 zinc-finger protein.

AAB39638.1 U68763 *Glycine max*
 putative transcription factor. SCOF-1. scof-1. zinc-finger protein.

CAB77055.1 Y18788 *Medicago sativa*
 putative TFIIIA (or kruppel)-like zinc finger protein.

AAC06243.1 AF053077 *Nicotiana tabacum*
 transcription factor. osmotic stress-induced zinc-finger protein. zfp.

BAA05077.1	D26084	Petunia x hybrida	zinc-finger DNA binding protein.
BAA05076.1	D26083	Petunia x hybrida	zinc-finger DNA binding protein.
AAB53260.1	U76554	Brassica rapa	transcription factor. zinc-finger protein-1. BR42.
BAA05078.1	D26085	Petunia x hybrida	zinc-finger DNA binding protein.
AAB53261.1	U76555	Brassica rapa	zinc-finger protein BcZFP1. BcZFP1(3-2z).
AAK01713.1	AF332876	Oryza sativa	zinc finger transcription factor ZF1.
BAA21920.1	AB006598	Petunia x hybrida	ZPT2-11. C2H2 zinc finger protein, 2finger.
BAA21922.1	AB006600	Petunia x hybrida	ZPT2-13. C2H2 zinc finger protein, 2finger.
BAA19112.1	AB000453	Petunia x hybrida	PETHy;ZPT3-1. Cys(2) His(2) zinc finger protein, 3 fingers.
BAA21927.1	AB006605	Petunia x hybrida	ZPT3-3. C2H2 zinc finger protein, 3 finger.
BAA96071.1	AB035133	Petunia x hybrida	C2H2 zinc-finger protein ZPT3-3. ZPT3-3.
BAA96070.1	AB035132	Petunia x hybrida	C2H2 zinc-finger protein ZPT2-10. PETHy;ZPT2-10.
BAA21919.1	AB006597	Petunia x hybrida	ZPT2-10. C2H2 zinc finger protein, 2 finger.
BAA19114.1	AB000455	Petunia x hybrida	PETHy;ZPT4-1. Cys(2) His(2) zinc finger protein, 4 fingers.
BAA21921.1	AB006599	Petunia x hybrida	ZPT2-12. C2H2 zinc finger protein, 2 finger.
BAA21928.1	AB006606	Petunia x hybrida	ZPT4-4. C2H2 zinc finger protein, 4 finger.
CAA60828.1	X87374	Pisum sativum	putative zinc finger protein.
BAA21925.1	AB006603	Petunia x hybrida	ZPT2-8. C2H2 zinc finger protein, 2 finger.
BAA19111.1	AB000452	Petunia x hybrida	PETHy;ZPT2-6. Cys(2) His(2) zinc finger protein, 2 fingers.
BAA19926.1	AB000456	Petunia x hybrida	PETHy; ZPT4-2. C2H2 zinc finger protein, 4 finger.
BAA21924.1	AB006602	Petunia x hybrida	ZPT2-7. C2H2 zinc finger protein, 2finger.

BAA21923.1 AB006601 *Petunia x hybrida*
ZPT2-14. C2H2 zinc finger protein, 2 finger.

BAA21926.1 AB006604 *Petunia x hybrida*
ZPT2-9. C2H2 zinc finger protein, 2 finger.

BAA19110.1 AB000451 *Petunia x hybrida*
PETHy;ZPT2-5. Cys(2) His(2) zinc finger protein, 2 fingers.

BAA19113.1 AB000454 *Petunia x hybrida*
PETHy;ZPT3-2. Cys(2) His(2) zinc finger protein, 3 fingers.

SEQ ID NO: 702

AAK29419.1 AF348319 *Zea mays*
TERMINAL EAR1. te1. RNA-binding protein; 3 putative RRM motifs; similar to
Schizosaccharomyces pombe Mei2 and Arabidopsis AML1; te1 cDNA sequence is presented
in GenBank Accession Number AF047852.

CAA57551.1 X82030 *Phaseolus vulgaris*
chloroplast RNA binding protein. RNP1.

CAA66479.1 X97905 *Vicia faba*
RNA- or ssDNA-binding protein.

CAC01237.1 AJ292767 *Nicotiana plumbaginifolia*
nuclear RNA binding protein. RNA Binding Protein 45. rbp45.

AAF66823.1 AF190655 *Nicotiana tabacum*
poly(A)-binding protein. PABP.

AAK30205.1 AF349964 *Daucus carota*
poly(A)-binding protein. Translin1P.

AAG59664.1 AC084319 *Oryza sativa*
putative RNA binding protein. OSJNBa0004B24.1.

AAB38974.1 U81318 *Triticum aestivum*
poly(A)-binding protein. wheatpab.

CAA81127.1 Z26042 *Anemia phyllitidis*
Binding to the poly(A)-tail of eukaryotic mRNAs. poly(A)-mRNA binding protein.

AAA79045.1 U34742 *Spinacia oleracea*
24 kDa RNA binding protein.

AAC39368.1 AF043297 *Chlamydomonas reinhardtii*
poly(A) binding protein RB47. PABP.

AAF63202.1 AF240679 *Cucumis sativus*
poly(A)-binding protein.

CAA11894.1 AJ224325 *Hordeum vulgare*
nucleic acid-binding protein. cp33Hv.

AAF66825.1 AF190657 *Nicotiana tabacum*
poly(A)-binding protein. PABP.

CAA06469.1 AJ005286 *Hordeum vulgare*
nucleic acid-binding protein. cp31AHv protein.

SEQ ID NO: 709

AAB36546.1 U77940 *Phaseolus vulgaris*
polyubiquitin. expression is regulated by heavy metal stress, UV, virus infection, heat shock
and wounding treatment, this suggests that ubiquitin plays a role in plant defense.

SEQ ID NO: 714

CAA61946.1 X89828 *Pisum sativum*
fructose-1,6-bisphosphate aldolase.

AAB61592.1 AF003124 *Mesembryanthemum crystallinum*
fructose-bisphosphate aldolase.

CAB77243.2 AJ133146 *Persea americana*
glycolytic enzyme, sixth step in glycolysis. fructose-bisphosphate aldolase. alf.

BAA08845.1 D50307 *Oryza sativa*
aldolase C-1.

BAA08830.1 D50301 *Oryza sativa*
aldolase C-1.

CAA46649.1 X65742 *Spinacia oleracea*
fructose-bisphosphate aldolase.

BAA02729.1 D13512 *Oryza sativa*
cytoplasmic aldolase.

AAG21429.1 AF308587 *Fragaria x ananassa*
cytosolic aldolase. SCA1.

CAA37290.1 X53130 *Oryza sativa*
fructose-diphosphate aldolase (AA 1-358).

CAA31366.1 X12872 *Zea mays*
fructose bisphosphate aldolase.

AAA33435.1 M16220 *Zea mays*
aldolase.

CAA61947.1 X89829 *Pisum sativum*
fructose-1,6-bisphosphate aldolase.

CAA06308.1 AJ005041 *Cicer arietinum*
cytosolic fructose-1,6-bisphosphate aldolase.

AAK19324.1 AF329673 *Dunaliella salina*
fructose-bisphosphate aldolase isoenzyme 1. salt-induced.

CAA71408.1 Y10380 *Solanum tuberosum*
homologous to plastidic aldolases.

BAA77603.1 AB027002 *Nicotiana paniculata*
plastidic aldolase.

BAA77604.1 AB027001 *Nicotiana paniculata*
plastidic aldolase NPALDP1. NpAldP1.

AAA33642.1 M97476 *Pisum sativum*
aldolase.

AAA33643.1 M97477 *Pisum sativum*
aldolase.

BAA02730.1	D13513	Oryza sativa	chloroplastic aldolase.
AAF74220.1	AF216582	Avena sativa	fructose 1,6-bisphosphate aldolase precursor.
CAA47293.1	X66814	Spinacia oleracea	fructose-bisphosphate aldolase.
AAK19325.1	AF329674	Dunaliella salina	fructose-bisphosphate aldolase isoenzyme 2. salt-induced.
CAB46520.1	AJ243524	Phleum pratense	sixth step in glycolysis. putative fructose-bisphosphate aldolase.
CAA09669.1	AJ011516	Scherffelia dubia	fructose-bisphosphate aldolase.
CAA49590.1	X69969	Chlamydomonas reinhardtii	fructose-bisphosphate aldolase. ALDCHL.
AAC60574.1	S72951	Chloroplast Chlamydomonas reinhardtii	fructosediphosphate aldolase. fructosediphosphate aldolase. This sequence comes from Fig. 4.
AAB70542.1	AF017362	Oryza sativa	aldolase.
BAA76430.1	AB025002	Cicer arietinum	fructose-bisphosphate aldolase.
AAD20818.1	AF107590	Dendrobium grex Madame Thong-In	putative fructose-bisphosphate aldolase. otg11.
BAA11395.1	D78500	Brassica rapa	putative aldolase. Sequence homologous to cytoplasmic aldolase of rice (D13512).
BAA78593.1	AU066535	Chlamydomonas sp. HS-5	fructose-bisphosphate aldolase precursor. NaCl inducible.
CAC34412.1	Y18576	Flaveria trinervia	fructose-bisphosphate aldolase. alf.
SEQ ID NO: 715			
AAK07429.1	AF321287	Musa acuminata	beta-glucosidase.
AAC69619.1	AF072736	Pinus contorta	beta-glucosidase.
AAF04007.1	AF163097	Dalbergia cochinchinensis	beta-fucosidase beta-glucosidase. dalcochinin 8'-O-beta-glucoside beta-glucosidase precursor. BGLU1. rotenoid beta-glucosidase.
AAA93032.1	U50201	Prunus serotina	hydrolysis of the cyanogenic glucoside (R)-prunasin. prunasin hydrolase precursor. located in protein bodies of Prunus seeds; encodes 8 putative N-glycosylation sites (N-X-S/T); encodes NEP and ITENG motifs characteristic of the BGA family of beta-glucosidases.
BAA78708.1	AB003089	Polygonum tinctorium	beta-glucosidase.

AAA91166.1	U39228	<i>Prunus avium</i>	beta-glucosidase.
BAA11831.1	D83177	<i>Costus speciosus</i>	saponin metabolite. furostanol glycoside 26-O-beta-glucosidase (F26G). functional expression in <i>E. coli</i> ; one of the F26G isozymes.
AAF34650.1	AF221526	<i>Prunus serotina</i>	hydrolysis of the cyanogenic glucoside (R)-prunasin. prunasin hydrolase isoform PHA precursor. beta-glucosidase; contains 6 potential N-glycosylation sites (N-X-S/T); glycosyl hydrolase family 1 member.
AAG25897.1	AF170087	<i>Cucurbita pepo</i>	silverleaf whitefly-induced protein 3. SLW3. similar to beta-glucosidase.
AAG00614.1	AF293849	<i>Secale cereale</i>	beta-glucosidase.
AAB22162.1	S35175	<i>Manihot esculenta</i>	linamarase. linamarase. beta-glucosidase; Method: conceptual translation with partial peptide sequencing; This sequence comes from Fig. 4.
AAF03675.1	AF149311	<i>Rauvolfia serpentina</i>	hydrolyses the glucoalkaloid raucaffricine. raucaffricine-O-beta-D-glucosidase. beta glucosidase; RG; part of the Ajmaline biosynthesis pathway; belongs to family 1 of the glucosyl hydrolases.
AAA87339.1	L41869	<i>Hordeum vulgare</i>	beta-glucosidase. BGQ60. expression specific to starchy endosperm of seed.
AAC49177.1	U33817	<i>Sorghum bicolor</i>	beta-glucosidase, catalyzes the hydrolysis of the cyanogenic beta-glucoside dhurrin. dhurrinase.
CAA64442.1	X94986	<i>Manihot esculenta</i>	beta glucosidase. bglA.
AAD02839.1	AF082991	<i>Avena sativa</i>	beta-D-glucosidase beta subunit precursor. P60b. avenacosidase.
AAD09850.1	U44087	<i>Zea mays</i>	beta-D-glucosidase precursor. glu2. product subunit structure: autodimer of 58.4 kDa monomers Allele: glu2-B73.
AAD10503.1	U33816	<i>Zea mays</i>	functions in defense of young plant parts against pests via the production of hydroxamic acids from hydroxamic acid glucosides. beta-D-glucosidase.
AAB03266.1	U44773	<i>Zea mays</i>	beta-D-glucosidase. glu1. autodimer of 58.4 kD monomers.
AAA65946.1	U25157	<i>Zea mays</i>	functions in defense of young plant parts against pests via the production of hydroxamic acids from hydroxamic acid glucosides. beta-D-glucosidase.
CAA52293.1	X74217	<i>Zea mays</i>	beta-glucosidase. p60.1.

AAF28800.1	AF112888	Catharanthus roseus	plays a role in secondary metabolism by hydrolyzing strictosidine to cathenamine during indole alkaloid biosynthesis. strictosidine beta-glucosidase. localized in the endoplasmic reticulum.
CAA40057.1	X56733	Trifolium repens	beta-glucosidase. Li.
CAA40058.1	X56734	Trifolium repens	beta-glucosidase. non-cyanogenic.
CAA55196.1	X78433	Avena sativa	beta-D-glucosidase.
CAA79989.2	Z21977	Brassica napus	beta thioglucosidase. myrosinase, thioglucoside glucohydrolase. Myr1.Bn1.
AAB71381.1	U95298	Manihot esculenta	linamarase. pLIN-GEN. beta-glucosidase.
CAA57913.1	X82577	Brassica napus	beta-glucosidase. bgl.
AAB38784.1	U72154	Brassica nigra	beta-glucosidase. psr3.1. PSR3.1; phosphate-starvation responsive enzyme.
AAF34651.1	AF221527	Prunus serotina	putative prunasin hydrolase precursor. beta-glucosidase; glycosyl hydrolase family 1 member.
AAA84906.1	U28047	Oryza sativa	catalyzes the release of either giberellin or cyanogenic substances from their glucoconjugates. beta glucosidase. beta-D-glucoside glucohydrolase; dimer of 60 kDa monomers; localized in the plastid.
CAC08209.1	AJ005950	Cicer arietinum	beta-glucosidase.
SEQ ID NO: 718			
AAF61647.1	AF190634	Nicotiana tabacum	UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.
BAA89009.1	AB027455	Petunia x hybrida	anthocyanin 5-O-glucosyltransferase. PH1.
BAA93039.1	AB033758	Citrus unshiu	limonoid UDP-glucosyltransferase. LGTase.
BAA36423.1	AB013598	Verbena x hybrida	UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.
BAA36421.1	AB013596	Perilla frutescens	UDP-glucose:anthocynin 5-O-glucosyltransferase. PF3R4.
AAF98390.1	AF287143	Brassica napus	catalyzes the transfer of glucose from UDP-glucose to sinapate and some other hydroxycinnamates (4-coumarate, caffate, ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.
BAA36422.1	AB013597	Perilla frutescens	UDP-glucose:anthocyanin 5-O-glucosyltransferase homologue. PF3R6.

BAB07962.1	AP002524	Oryza sativa	putative anthocyanin 5-O-glucosyltransferase. P0406H10.16. contains ESTs AU067881(C10481),AU067882(C10481).
AAD21086.1	AF127218	Forsythia x intermedia	adds glucose residue to position 3 of flavonoid compounds. flavonoid 3-O-glucosyltransferase. UFGT.
AAK16178.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.5.
BAA12737.1	D85186	Gentiana triflora	UDP-glucose:flavonoid-3-glucosyltransferase.
AAK16181.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.16.
AAK16175.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.15.
AAK16172.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.14.
CAA59450.1	X85138	Lycopersicon esculentum	twil. homologous to glucosyltransferases.
AAF17077.1	AF199453	Sorghum bicolor	UDP-glucose glucosyltransferase. UDP-glucose:p-hydroxymandelonitrile-o-glucosyltransferase.
BAA89008.1	AB027454	Petunia x hybrida	anthocyanidin 3-O-glucosyltransferase. PGT8.
AAB81683.1	AF000372	Vitis vinifera	UDP glucose:flavonoid 3-o-glucosyltransferase.
BAB41017.1	AB047090	Vitis labrusca x Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT1. The gene was derived from one of the parents V. labruscana cv. Ishiharawase.
AAB81682.1	AF000371	Vitis vinifera	UDP glucose:flavonoid 3-o-glucosyltransferase.
BAB41022.1	AB047095	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT2.
BAB41020.1	AB047093	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT2.
BAB41021.1	AB047094	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT1.
BAB41019.1	AB047092	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT1.
BAA83484.1	AB031274	Scutellaria baicalensis	UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.
BAB41025.1	AB047098	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT1.

BAB41023.1	AB047096	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT1.
BAA90787.1	AB038248	Ipomoea batatas	UDP glucose: flavonoid 3-O-glucosyltransferase. uf3gt.
BAA19659.1	AB002818	Perilla frutescens	flavonoid 3-O-glucosyltransferase. UDP glucose.
BAB41018.1	AB047091	Vitis labrusca x Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT2. The gene originated in one of the parents V. vinifera cv. Centennial.
AAB36652.1	U32643	Nicotiana tabacum	immediate-early salicylate-induced glucosyltransferase. IS10a.
AAK28304.1	AF346432	Nicotiana tabacum	phenylpropanoid:glucosyltransferase 2. togt2. glucosyltransferase.
BAB41024.1	AB047097	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT2.
BAB41026.1	AB047099	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT2.
CAA31855.1	X13500	Zea mays	UDPglucose:flavonol 3-O-glucosyltransferase.
AAB86473.1	AF028237	Ipomoea purpurea	UDP glucose: flavonoid 3-O-glucosyltransferase. UF3GT-FL1.
CAA54614.1	X77464	Manihot esculenta	UTP-glucose glucosyltransferase. CGT7.
SEQ ID NO: 719			
AAC24195.1	AF020425	Nicotiana tabacum	calmodulin binding protein. glutamate decarboxylase isozyme 1. NtGAD1. calcium-calmodulin-dependent enzyme.
AAK18620.1	AF352732	Nicotiana tabacum	converts glutamate to gamma-aminobutyric acid. glutamate decarboxylase isozyme 3. GAD; GAD3; NtGAD3; calcium/calmodulin-dependent enzyme.
AAB40608.1	U54774	Nicotiana tabacum	glutamate decarboxylase. NtGAD1. calmodulin regulated enzyme; calmodulin-binding protein.
AAA33710.1	L16977	Petunia x hybrida	glutamate decarboxylase. gad.
AAA33709.1	L16797	Petunia x hybrida	glutamate decarboxylase. gad.
AAC39483.1	AF020424	Nicotiana tabacum	glutamate decarboxylase isozyme 2. NtGAD2. calcium-calmodulin-dependent enzyme.
BAB32870.1	AB056062	Oryza sativa	glutamate decarboxylase. GAD.
BAB32868.1	AB056060	Oryza sativa	glutamate decarboxylase. GAD.

CAA56812.1 X80840 *Lycopersicon esculentum*
homology to pyroxidial-5'-phosphate-dependant glutamate decarboxylases; putative start codon.

BAB32871.1 AB056063 *Oryza sativa*
glutamate decarboxylase. GAD.

BAB32869.1 AB056061 *Oryza sativa*
glutamate decarboxylase. GAD.

CAA50719.1 X71900 *Lycopersicon esculentum*
histidine decarboxylase. hdc. pyridoxal 5'-phosphate dependant.

SEQ ID NO: 720

BAA92713.1 AP001389 *Oryza sativa*
ESTs AU033035(S1515),D39871(S1515) correspond to a region of the predicted gene. Similar to *Arabidopsis thaliana* chromosome II BAC F22D22 genomic sequence; putative glucan synthase (AC006223).

AAD25952.1 AF085717 *Gossypium hirsutum*
putative callose synthase catalytic subunit. CFL1. cotton FKS1-like protein; similar to *Saccharomyces cerevisiae* beta-1,3-glucan synthase subunit FKS1.

SEQ ID NO: 721

CAB55396.1 AL117264 *Oryza sativa*
zwh12.1. similar to *Arabidopsis* putative UDP-galactase-4-epimerase (AC007060); Method: conceptual translation with partial peptide sequencing.

CAA06339.1 AJ005082 *Cyamopsis tetragonoloba*
UDP-galactose 4-epimerase.

AAA86532.1 U31544 *Pisum sativum*
catabolism of galactose to glucose in Leloir pathway, and in galactose synthesis from glucose. UDP-galactose-4-epimerase. galE. galactowaldenase.

CAA06338.1 AJ005081 *Cyamopsis tetragonoloba*
UDP-galactose 4-epimerase.

BAB40967.1 AB059568 *Pisum sativum*
biosynthesis of UDP-D-xylose. UDP-D-glucuronate carboxy-lyase. uxs1.

SEQ ID NO: 726

BAA88198.1 AP000837 *Oryza sativa*
Similar to human dimethylaniline monooxygenase (AC002376).

BAA35120.1 AB008845 *Oryza sativa*
NADH dependent Glutamate Synthase.

AAB41904.1 L37606 *Medicago sativa*
NADH-dependent glutamate synthase.

BAA88195.1 AP000837 *Oryza sativa*
Similar to human dimethylaniline monooxygenase (AC002376).

AAB46617.1 L01660 *Medicago sativa*

the 3 cysteine residues in this region (amino acid residues 1246-1257) may serve to coordinate the [3Fe-4S] cluster that is probably found in this protein. See Knaff et al. (1991) J. Biol. Chem.266:150. NADH-glutamate synthase. NADH-GOGAT; activity increases dramatically during nodule development; the 3 cysteine residues in this region may serve to coordinate the [3Fe-4S] cluster that is probably found in this protein. See Knaff et al. (1991) J. Biol. Chem.266:15080-15084.

SEQ ID NO: 728

AAG43550.1 AF211532 *Nicotiana tabacum*

Avr9/Cf-9 rapidly elicited protein 132. ACRE132. similar to RING finger proteins.

BAA96875.1 AB045121 *Oryza sativa*

RING finger 1. RRF1.

AAK00436.1 AC060755 *Oryza sativa*

putative zinc finger protein. OSJNBa0003O19.23.

BAA78746.1 AB023482 *Oryza sativa*

Similar to Arabidopsis thaliana RING-H2 finger protein RHX1a mRNA, partial cds.(AF079184).

CAA74911.1 Y14573 *Hordeum vulgare*

ring finger protein. putative.

AAG46117.1 AC073166 *Oryza sativa*

putative ring finger protein. OSJNBb0064P21.7.

BAA85438.1 AP000616 *Oryza sativa*

similar to RING-H2 finger protein RHA1a (AF078683).

BAA77204.1 AB026262 *Cicer arietinum*

ring finger protein.

SEQ ID NO: 730

AAA86424.1 U44386 *Lycopersicon esculentum*

heat shock protein. TFHS1. similar to protein encoded by the arg2 gene in mung bean, encoded by Genbank Accession Number D14411.

SEQ ID NO: 731

CAA06756.1 AJ005899 *Nicotiana tabacum*

G subunit. G subunit of Vacuolar-type H⁺-ATPase. vag1.

CAA06757.1 AJ005900 *Nicotiana tabacum*

Subunit G of vacuolar-type H⁺-ATPase. vag2. vag2.

AAD56039.1 AF184068 *Citrus limon*

vacuolar membrane ATPase subunit G. LVMA10. V-ATPase VMA10.

SEQ ID NO: 737

AAF69008.1 AF257779 *Oryza sativa*

stress-inducible protein. OsSII.

SEQ ID NO: 739

CAC12996.1 AJ299398 *Medicago truncatula*

putative auxin import. putative AUX1-like permease. lax2.

AAF21982.1	AF115543	Populus tremula x Populus tremuloides
AUX1-like protein. PAX1.		
AAG17171.1	AF190880	Populus tremula x Populus tremuloides
putative AUX1-like permease. pax5.		
CAC12995.1	AJ299397	Medicago truncatula
putative auxin import. putative AUX1-like permease. lax1.		
CAC12997.1	AJ299399	Medicago truncatula
putative auxin import. putative AUX1-like permease. lax3.		
CAB65535.1	AJ011794	Zea mays
AUX1 protein. aux1.		

SEQ ID NO: 740

CAA65269.1	X96406	Solanum tuberosum
13-lipoxygenase.		
AAB65767.1	U37840	Lycopersicon esculentum
lipoxygenase. loxD. wound, systemin and methyl-jasmonate induced.		
BAA03102.1	D14000	Oryza sativa
lipoxygenase. lox2osPil.		
AAC12951.1	U56406	Hordeum vulgare
methyljasmonate-inducible lipoxygenase 2.		
CAB94852.1	AJ404331	Prunus dulcis
hydroperoxydation of polyunsaturated fatty acids. lipoxygenase. lox.		
AAG21691.1	AY008278	Lycopersicon esculentum
lipoxygenase. oxido-reductase.		
AAA79186.1	U36339	Cucumis sativus
lipoxygenase.		
AAB67858.1	U60200	Solanum tuberosum
lipoxygenase. POTLX-1. expressed during early tuberization.		
CAA64765.1	X95512	Solanum tuberosum
lipoxygenase.		
CAB83038.1	AJ271161	Cucumis sativus
oxygenase. lipoxygenase-9. lox9.		
CAA58859.1	X84040	Nicotiana tabacum
lipoxygenase. Lox1.		
AAB67865.1	U60202	Solanum tuberosum
lipoxygenase. POTLX-3. expressed in ABA-treated leaves.		
CAA55724.1	X79107	Solanum tuberosum
lipoxygenase. Lox1:St:1.		
AAB67860.1	U60201	Solanum tuberosum
lipoxygenase. POTLX-2. expressed during early tuberization.		
CAB65460.1	Y18548	Solanum tuberosum
lipoxygenase. lox1-St-2.		

AAD04258.1	AF039651	Solanum tuberosum	5-lipoxygenase.
AAB81594.1	AF019613	Solanum tuberosum	lipoxygenase. plox1.
AAA33986.1	J02795	Glycine max	lipoxygenase-1.
AAB67732.1	U50075	Glycine max	lipoxygenase L-5. vlxB.
CAA47717.1	X67304	Glycine max	lipoxygenase.
AAB81595.1	AF019614	Solanum tuberosum	lipoxygenase. plox2.
CAA64766.1	X95513	Solanum tuberosum	lipoxygenase.
AAB31252.1	S73865	Solanum tuberosum	linoleate:oxygen oxidoreductase. linoleate:oxygen oxidoreductase, lipoxygenase, LOX. This sequence comes from Fig. 1; lipoxygenase; LOX.
AAA53184.1	U09026	Lycopersicon esculentum	lipoxygenase. loxA.
AAB65766.1	U37839	Lycopersicon esculentum	lipoxygenase. loxC. expressed during ripening fruit.
CAA65268.1	X96405	Solanum tuberosum	13-lipoxygenase.
AAF15296.2	AF204210	Phaseolus vulgaris	lipoxygenase. LOX4.
CAA55319.1	X78581	Pisum sativum	lipoxygenase. Lox1:Ps:3.
AAA03728.1	U04526	Glycine max	lipoxygenase.
CAA34906.1	X17061	Pisum sativum	lipoxygenase (AA 1-864).
CAA55318.1	X78580	Pisum sativum	lipoxygenase. Lox1:Ps:2.
BAA03042.1	D13949	Glycine max	lacking. lipoxygenase-2. lox2.
AAA33987.1	J03211	Glycine max	lipoxygenase (EC 1.13.11.12).
AAB71759.1	U84198	Pisum sativum	lipoxygenase. Lox1:Ps:1. expressed in root nodules.
AAB41272.1	U50081	Glycine max	lipoxygenase-3.
CAA39604.1	X56139	Glycine max	lipoxygenase. sc514.

AAA96817.1	U26457	Glycine max lipoxygenase. vlxC.
AAG42354.1	AF234983	Phaseolus vulgaris lipoxygenase.
AAG18376.1	AF283894	Zantedeschia aethiopica lipoxygenase. lox2.
AAD39093.1	AF095895	Oryza sativa catalyzes the addition of molecular oxygen to fatty acid. lipoxygenase. CM-LOX1.
CAC04380.1	AJ293015	Pisum sativum lipoxygenase. lox1:Ps:7.
CAA45088.1	X63525	Phaseolus vulgaris lipoxygenase. loxA.
AAB18970.2	U76687	Phaseolus vulgaris lipoxygenase. PvLOX2.
AAC49159.1	U36191	Glycine max linoleate:oxygen oxidoreductase. lipoxygenase. lox7.
AAA03726.1	U04785	Glycine max lipoxygenase.
CAA45086.1	X63521	Phaseolus vulgaris lipoxygenase.

SEQ ID NO: 741

AAG28436.1	AF195029	Glycine max plasma membrane Ca ²⁺ -ATPase. SCA2.
AAG28435.1	AF195028	Glycine max plasma membrane Ca ²⁺ -ATPase. SCA1.
CAA68234.1	X99972	Brassica oleracea calmodulin-stimulated calcium-ATPase.
AAD31896.1	AF145478	Mesembryanthemum crystallinum calcium ATPase.
BAA90510.2	AP001111	Oryza sativa rice EST AU030811, similar to rice Ca ²⁺ -ATPase (U82966).
AAD11618.1	AF050496	Lycopersicon esculentum Ca ²⁺ -ATPase. LCA1B; alternative transcript.
AAD11617.1	AF050495	Lycopersicon esculentum Ca ²⁺ -ATPase. LCA1A; alternative transcript.
AAA34138.1	M96324	Lycopersicon esculentum The calcium ATPase is a calcium ion pump. Ca ²⁺ -ATPase. LCA1.
CAA63790.1	X93592	Dunaliella bioculata P-type ATPase. cal. calcium pumping; CA1.
AAF73985.1	AF096871	Zea mays calcium pump. calcium ATPase. cap1.

AAB58910.1	U82966	Oryza sativa	Ca ²⁺ -ATPase.
AAD46188.1	AF156691	Nicotiana plumbaginifolia	plasma membrane proton ATPase. pma9.
AAB17186.1	U72148	Lycopersicon esculentum	plasma membrane H ⁺ -ATPase. LHA4. plasma membrane proton pumping ATPase.
CAA47275.1	X66737	Nicotiana plumbaginifolia	plasma membrane H ⁺ -ATPase. pma4.
CAA54045.1	X76535	Solanum tuberosum	H ⁽⁺⁾ -transporting ATPase. PHA2.
AAD46186.1	AF156679	Nicotiana plumbaginifolia	plasma membrane proton ATPase. pma6.
CAA59800.1	X85805	Zea mays	H ⁽⁺⁾ -transporting ATPase. MHA-2.
BAA06629.1	D31843	Oryza sativa	plasma membrane H ⁺ -ATPase. OSA2.
AAB35314.2	S79323	Vicia faba	plasma membrane H ⁽⁺⁾ -ATPase precursor. plasma membrane H ⁽⁺⁾ -ATPase. This sequence comes from Fig. 1; conceptual translation presented here differs from translation in publication.
CAA59799.1	X85804	Phaseolus vulgaris	H ⁽⁺⁾ -transporting ATPase. BHA-1.
AAB41898.1	U84891	Mesembryanthemum crystallinum	plasma membrane proton pump. H ⁺ -transporting ATPase. PMA.
AAA34094.1	M80489	Nicotiana plumbaginifolia	plasma membrane H ⁺ ATPase. pma1.
AAB84202.2	AF029256	Kosteletzkya virginica	plasma membrane proton ATPase. ATP1.
AAA34052.1	M27888	Nicotiana plumbaginifolia	H ⁺ -translocating ATPase.
AAA34173.1	M60166	Lycopersicon esculentum	H ⁺ -ATPase. LHA1.
AAA34098.1	M80490	Nicotiana plumbaginifolia	plasma membrane H ⁺ ATPase. pma3.
AAF98344.1	AF275745	Lycopersicon esculentum	plasma membrane H ⁺ -ATPase. LHA2. P-type ion pump.
AAD55399.1	AF179442	Lycopersicon esculentum	plasma membrane H ⁺ -ATPase isoform LHA2. LHA2.
CAC29436.1	AJ310524	Vicia faba	P-type H ⁺ -ATPase. ha5. predominantly expressed in guard cells and flowers.
BAA08134.1	D45189	Zostera marina	plasma membrane H ⁺ -ATPase. zha1.

BAA01058.1	D10207	Oryza sativa	H-ATPase. OSA1.
CAB69824.1	AJ271439	Prunus persica	plasma membrane H ⁺ ATPase. PPA1.
CAA54046.1	X76536	Solanum tuberosum	H(+)-transporting ATPase. PHA1.
AAB60276.1	U09989	Zea mays	H(+)-transporting ATPase. Mha1.
CAB69823.1	AJ271438	Prunus persica	plasma membrane H ⁺ ATPase. PPA2.
AAK31799.1	AY029190	Lilium longiflorum	plasma membrane H ⁺ ATPase. LILHA1.
BAA37150.1	AB022442	Vicia faba	p-type H ⁺ -ATPase. VHA2.
CAC29435.1	AJ310523	Vicia faba	P-type H ⁺ -ATPase. vha4. predominantly expressed in flowers.
CAB85495.1	AJ132892	Medicago truncatula	proton pump. H ⁺ -ATPase. ha1.
CAB85494.1	AJ132891	Medicago truncatula	proton pump. H ⁺ -ATPase. ha1.
AAD46187.1	AF156683	Nicotiana plumbaginifolia	plasma membrane proton ATPase. pma8.
AAD29712.1	AF140499	Oryza sativa	chloroplast envelope calcium ATPase precursor.
AAK32118.1	AF308816	Hordeum vulgare	plasmalemma H ⁺ -ATPase 1.
AAG01028.1	AF289025	Cucumis sativus	plasma membrane H ⁺ -ATPase.
AAF97591.1	AF263917	Lycopersicon esculentum	plasma membrane proton ATPase. LHA8.
AAA81348.1	U38965	Vicia faba	p-type H ⁺ -ATPase. VHA2.
AAA20600.1	U08984	Zea mays	plasma-membrane H ⁺ ATPase. Zmpma1.
AAA20601.1	U08985	Zea mays	plasma-membrane H ⁺ ATPase. Zmpma1.
AAK32119.1	AF308817	Hordeum vulgare	plasmalemma H ⁺ -ATPase 2.
SEQ ID NO: 742			
AAD02548.1	AF049922	Petunia x hybrida	PGPS/D6. PGPS/D6. ER lumen protein retaining receptor homolog; putative HDEL receptor.
SEQ ID NO: 744			

AAG13424.1 AC051634 *Oryza sativa*
putative mitochondrial inner membrane protein. OSJNBb0018B10.5.

AAG46068.1 AC079830 *Oryza sativa*
putative inner mitochondrial membrane protein. OSJNBb0009F04.14.

SEQ ID NO: 746

BAA32557.1 AB017159 *Daucus carota*
citrate synthase. DcCS.

AAA82743.1 U19481 *Citrus maxima*
synthesis of citrate from oxaloacetate and acetylCoA. citrate synthase precursor. cit.

AAG28777.1 AF302906 *Oryza sativa*
citrate synthase. similar to putative *Oryza sativa* citrate synthase in GenBank Accession Number AC004521.

CAA59008.1 X84226 *Nicotiana tabacum*
citrate synthase. cit1.

CAA52976.1 X75082 *Solanum tuberosum*
mitochondrial citrate-synthase. ethanolamine ammonia-lyase.

BAA82390.1 AP000367 *Oryza sativa*
ESTs C96653(C10531),C96654(C10531),C28571(C61641) correspond to a region of the predicted gene.; Similar to citrate synthetase. (AC004521).

CAA59010.1 X84228 *Beta vulgaris*
citrate (si)-synthase. cit1.

CAA59009.1 X84227 *Populus x generosa*
citrate (si)-synthase. cit1.

BAA07328.1 D38132 *Cucurbita* sp.
conversion of oxaloacetate to citrate in the glyoxylate cycle. glyoxysomal citrate synthase.

SEQ ID NO: 750

AAA85365.1 L42466 *Picea glauca*
ethylene-forming enzyme. EFE.

AAC95363.1 AF104925 *Solanum chacoense*
2-oxoglutarate-dependent dioxygenase. SPP2. pollination and fertilization induced gene.

BAA75309.1 AB023790 *Ipomoea batatas*
flavanone 3-hydroxylase. f3h III.

BAA75308.1 AB023789 *Ipomoea batatas*
flavanone 3-hydroxylase. f3h II.

BAA75306.1 AB023787 *Ipomoea batatas*
anthocyanidin synthase. ans II.

AAC48922.1 U06047 *Vigna radiata*
1-aminocyclopropane-1-carboxylate oxidase homolog.

SEQ ID NO: 751

BAB40010.1 AP003021 *Oryza sativa*
putative wall-associated kinase 2. P0503E05.12.

BAA95893.1 AP002071 *Oryza sativa*
Similar to *Arabidopsis thaliana* wak4 gene; wall-associated kinase 4. (AJ009695).

BAB40015.1	AP003021	Oryza sativa	putative wall-associated kinase 1. P0503E05.18.
BAA92221.1	AP001278	Oryza sativa	Similar to Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).
BAA87852.1	AP000816	Oryza sativa	Similar to putative Ser/Thr protein kinase. (AC004218).
BAB40021.1	AP003021	Oryza sativa	putative wall-associated kinase 2. P0503E05.25. contains EST C24950(S16264).
CAB51834.1	00069	Oryza sativa	11332.5. contains eukaryotic protein kinase domain PF.
AAB09771.1	U67422	Zea mays	CRINKLY4 precursor. cr4. receptor kinase homolog.
BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
AAK11566.1	AF318490	Lycopersicon hirsutum	Pto-like protein kinase E. LhirPtoE. confers resistance to bacterial speck disease.
BAB39409.1	AP002901	Oryza sativa	putative protein kinase. P0456F08.9. contains EST C23560(R0290).
BAB21240.1	AP002953	Oryza sativa	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
BAB40022.1	AP003021	Oryza sativa	putative wall-associated kinase 1. P0503E05.26.
CAA97692.1	Z73295	Catharanthus roseus	receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
BAB16871.1	AP002537	Oryza sativa	putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
AAK11674.1	AF339747	Lophopyrum elongatum	protein kinase. ESI47.
AAF43496.1	AF131222	Lophopyrum elongatum	protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.
BAA90808.1	AP001168	Oryza sativa	Similar to putative receptor-like protein kinase (AL035679).
AAF76313.1	AF220603	Lycopersicon esculentum	Pto kinase. LescPth5.
AAB47421.1	U59316	Lycopersicon esculentum	serine/threonine protein kinase Pto. pto. allele of Pto bacterial speck disease resistance gene in tomato.

AAB47423.1	U59315	<i>Lycopersicon pimpinellifolium</i> serine/threonine protein kinase Pto. Pto. bacterial speck disease resistance in tomato; disease resistance gene.
AAC48914.1	U02271	<i>Lycopersicon pimpinellifolium</i> protein kinase.
AAF76306.1	AF220602	<i>Lycopersicon pimpinellifolium</i> Pto kinase.
AAG59657.1	AC084319	<i>Oryza sativa</i> putative protein kinase. OSJNBa0004B24.20.
AAK11567.1	AF318491	<i>Lycopersicon hirsutum</i> Pto-like protein kinase F. LhirPtoF.
AAK21965.1	AY028699	<i>Brassica napus</i> receptor protein kinase PERK1.
AAG25966.1	AF302082	<i>Nicotiana tabacum</i> cytokinin-regulated kinase 1. CRK1. protein kinase; transcript abundance decreases rapidly after cytokinin treatment.
AAK11569.1	AF318493	<i>Lycopersicon hirsutum</i> Pto-like protein kinase D. LhirPtoD.
AAF66615.1	AF142596	<i>Nicotiana tabacum</i> LRR receptor-like protein kinase.
AAG03090.1	AC073405	<i>Oryza sativa</i> Similar to an <i>Arabidopsis</i> somatic embryogenesis receptor-like kinase (AC007504).
BAA87853.1	AP000816	<i>Oryza sativa</i> EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
BAA83373.1	AP000391	<i>Oryza sativa</i> ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).
BAA84787.1	AP000559	<i>Oryza sativa</i> ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).
CAA74662.1	Y14286	<i>Brassica oleracea</i> SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
CAA67145.1	X98520	<i>Brassica oleracea</i> receptor-like kinase. SFR2.
CAA73133.1	Y12530	<i>Brassica oleracea</i> serine /threonine kinase. ARLK.
AAK11568.1	AF318492	<i>Lycopersicon hirsutum</i> Pto-like protein kinase B. LhirPtoB.
BAA78764.1	AB023482	<i>Oryza sativa</i> ESTs C98382(C2985),D22444(C11129) correspond to a region of the predicted gene.; Similar to <i>Arabidopsis thaliana</i> APK1 gene for protein tyrosine-serine-threonine kinase.(D12522).

AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.
AAK31267.1	AC079890	Oryza sativa	putative protein kinase. OSJNBb0089A17.2.
BAA94509.1	AB041503	Populus nigra	protein kinase 1. PnPK1.
BAA94510.1	AB041504	Populus nigra	protein kinase 2. PnPK2.
SEQ ID NO: 752			
BAB39155.1	AB048713	Pisum sativum	SCARECROW. PsSCR.
AAG13663.1	AF263457	Zea mays	transcription factor. SCARECROW. SCR. ZmSCR.
BAA90816.1	AP001168	Oryza sativa	Similar to SCARECROW (U62798).
AAC98090.1	AF067400	Zea mays	Sc11 protein. Sc11. Scarecrow-like; similar to Zea mays sequence presented in GenBank Accession Number T18310.
BAB39156.1	AB048714	Pisum sativum	SCARECROW. PsSCR.
SEQ ID NO: 753			
AAF21901.1	AF109392	Brassica napus	ligand gated channel-like protein. glutamate receptor homolog.
SEQ ID NO: 757			
CAA92821.1	Z68504	Oryza sativa	3-hydroxy-3-methylglutaryl-CoA reductase.
AAA33360.1	M74800	Hevea brasiliensis	3-hydroxy-3-methylglutaryl-coenzyme A reductase. hmgr3.
CAA70440.1	Y09238	Zea mays	3-hydroxy-3-methylglutaryl coenzyme A reductase.
AAB69727.1	U72146	Camptotheca acuminata	3-hydroxy-3-methylglutaryl coenzyme A reductase. converts HMGCoA in mevalonate precursor for isoprenoid compounds; HMGR; hmg2; similar to protein encoded by GenBank Accession Number L10390.
AAD08820.1	U43961	Oryza sativa	3-hydroxy-3-methylglutaryl-CoA reductase. HMGR.
AAA68965.1	U14624	Artemisia annua	3-hydroxy-3-methylglutaryl coenzyme A reductase. AHM1.
AAD47596.1	AF142473	Artemisia annua	HMG-CoA reductase. HMGR1.
AAD03789.1	U43711	Morus alba	catalyzes the final step in mevalonate pathway. 3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMGR.

AAA33108.1	M96068	Catharanthus roseus	hydroxymethylglutaryl-CoA reductase. HMGR.
CAA48610.1	X68651	Raphanus sativus	hydroxymethylglutaryl-CoA reductase (NADPH). HMG1.
AAA93498.1	L01400	Solanum tuberosum	convert HMG-CoA into mevalonate. hydroxymethylglutaryl coenzyme A reductase. hmgr. putative.
AAA68966.1	U14625	Artemisia annua	3-hydroxy-3-methylglutaryl coenzyme A reductase. AHM4.
AAB52552.1	U51986	Solanum tuberosum	HMG-CoA reductase.
CAA48611.1	X68652	Raphanus sativus	hydroxymethylglutaryl-CoA reductase (NADPH). HMG2.
BAA93631.1	AB022690	Solanum tuberosum	3-hydroxy-3-methylglutaryl coenzyme A reductase. HMG3.
AAB62581.1	U68072	Lycopersicon esculentum	3-hydroxy-3-methylglutaryl CoA reductase 2. HMG2.
AAA34169.1	M63642	Lycopersicon esculentum	3-hydroxy-3-methylglutaryl coenzyme A reductase. hmg2.
AAB69726.1	U72145	Camptotheca acuminata	converts HMGC CoA to mevalonate. 3-hydroxy-3-methylglutaryl coenzyme a reductase. hmg3. HMGR.
AAB52551.1	U51985	Solanum tuberosum	HMG-CoA reductase.
AAA33040.1	L10390	Camptotheca acuminata	3-hydroxy-3-methylglutaryl coA reductase.
AAD28179.1	AF110383	Capsicum annuum	3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMGR2M. HMGR.
BAB20771.1	AB041031	Solanum tuberosum	3-hydroxy-3-methylglutaryl coenzyme A reductase. HMG2.
AAB53748.1	U95816	Oryza sativa	3-hydroxy-3-methylglutaryl-CoA reductase. HMGR.
AAC05088.1	AF038045	Gossypium hirsutum	catalyzes the synthesis of mevalonate from hmg-coA. 3-hydroxy-3-methylglutaryl-coenzyme A reductase 1. hmg1. hmg-coA reductase 1; HMGR1.
CAA45181.1	X63649	Nicotiana glauca	catalyses synthesis of mevalonate. 3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMGR. endoplasmic reticulum location.
CAA38469.1	X54659	Hevea brasiliensis	hydroxymethylglutaryl-CoA reductase. HMGR1.
CAA38467.1	X54657	Hevea brasiliensis	hydroxymethylglutaryl-CoA reductase. HMGR1.

AAD38873.1	AF110382	Oryza sativa	3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMGR3G. HMG-CoA reductase.
BAA36291.1	AB021862	Cucumis melo	HMG-CoA reductase. Cm-HMGR. putative.
AAB87727.1	U60452	Nicotiana tabacum	hydroxy-methylglutaryl-coenzyme A reductase. HMGR1.
AAC05089.1	AF038046	Gossypium hirsutum	catalyzes the synthesis of mevalonate from hmg-coA. 3-hydroxy-3-methylglutaryl-coenzyme A reductase 2. hmg2. hmg-coA reductase 2; HMGR2.
AAC15475.1	AF034760	Tagetes erecta	3-hydroxy-3-methylglutaryl coenzyme A reductase.
AAC15476.1	AF034761	Tagetes erecta	3-hydroxy-3-methylglutaryl coenzyme A reductase.
AAA21720.1	L28995	Oryza sativa	conversion of hydroxymethylglutaryl coenzyme A to mevalonate. 3-hydroxy-3-methylglutaryl coenzyme A reductase. putative.
AAA33358.1	M74798	Hevea brasiliensis	3-hydroxy-3-methylglutaryl-coenzyme A reductase. hmgr3.
AAC72378.1	AF096838	Solanum tuberosum	3-hydroxy-3-methylglutaryl coenzyme A reductase.
AAB04043.1	L40938	Lycopersicon esculentum	HMGR CoA reductase. HMGR1.
CAA38468.1	X54658	Hevea brasiliensis	hydroxymethylglutaryl-CoA reductase. HMGR2.
CAA52787.1	X74783	Lithospermum erythrorhizon	3-hydroxy-3-methyl glutaryl coenzyme A reductase. Lehmgr1.
AAD09278.1	U97683	Glycine max	catalyzes the synthesis of mevalonate, the specific precursor of all isoprenoid compounds present in plants. 3-hydroxy-3-methylglutaryl-coenzyme A reductase. HMG-CoA reductase.
AAG43469.1	AF196964	Bixa orellana	catalyzes mevalonate synthesis from hmg-CoA. 3-hydroxy-3-methylglutaryl-coenzyme A reductase.
BAA09705.1	D63389	Cucumis sativus	3-hydroxy-3-methylglutaryl CoA reductase.
AAB47161.1	S82272	Gossypium barbadense	3-hydroxy-3-methylglutaryl coenzyme A reductase. /gene="3-hydroxy-3-methylglutaryl coenzyme A reductase,. This sequence comes from Fig. 2; 3-hydroxy-3-methylglutaryl CoA reductase; HMGR.
AAA33359.1	M74799	Hevea brasiliensis	3-hydroxy-3-methylglutaryl-coenzyme A reductase. hmgr3.
AAC37434.1	L34827	Solanum tuberosum	HMG-CoA reductase. hmg1 gene family.

AAC37432.1	L34825	Solanum tuberosum	HMG-CoA reductase. hmg1 gene family.
AAC37435.1	L34828	Solanum tuberosum	HMG-CoA reductase. hmg1 gene family.
AAC37433.1	L34826	Solanum tuberosum	HMG-CoA reductase. hmg1 gene family.
AAC37431.1	L34823	Solanum tuberosum	HMG-CoA reductase. hmg1 gene family.
SEQ ID NO: 761			
CAA96512.1	Z71980	Malus x domestica	knotted1-like homeobox protein.
BAA25921.1	AB004797	Nicotiana tabacum	NTH23. homeobox gene.
AAD09582.1	U76409	Lycopersicon esculentum	homeobox 1 protein. THox1. homeodomain protein.
AAC49918.1	AF000142	Lycopersicon esculentum	class II knotted-like homeodomain protein. LeT12.
BAA08552.1	D49704	Oryza sativa	OSH45. OSH44 transcript homeobox gene.
BAB18585.1	AB043957	Ceratopteris richardii	CRKNOX3. crknox3. knotted1-like homeodomain protein.
AAD00253.1	U76410	Lycopersicon esculentum	homeobox 2 protein. THox2. homeodomain protein.
CAA82314.1	Z29073	Brassica napus	homeodomain-containing protein. Bnhd1.
BAA77822.1	AB007628	Oryza sativa	HOS59. homeobox gene.
BAA77823.1	AB007629	Oryza sativa	HOS66. homeobox gene.
AAB81079.1	AF022390	Hordeum vulgare	knotted class 1 homeodomain protein. k. similar to the hooded gene product encoded by GenBank Accession Number X83518; similar to the maize knotted-1 gene product encoded by GenBank Accession Number X61308.
AAF32399.1	AF224499	Triticum aestivum	KNOTTED-1-like homeobox protein b. knox1b. KNOX1b.
BAA76750.1	AB025573	Nicotiana tabacum	KN1-type homeobox protein. NTH1.
AAF32400.1	AF224500	Triticum aestivum	KNOTTED-1-like homeobox protein d. knox1d. KNOX1d.
AAC49917.1	AF000141	Lycopersicon esculentum	class I knotted-like homeodomain protein. LeT6.
BAA25546.1	AB004785	Nicotiana tabacum	NTH15. homeobox gene.

AAF32398.1	AF224498	Triticum aestivum	KNOTTED-1-like homeobox protein a. knox1a. KNOX1.
AAD13611.1	AF100455	Zea mays	knotted class 1 homeodomain protein liguleless3. lg3.
AAC84001.1	AF063248	Picea abies	homeobox protein.
AAC33008.1	AF080104	Pisum sativum	knotted1-like class I homeodomain protein. PsKn1.
AAD00692.1	U90092	Picea mariana	homeobox transcription factor SKN2. knotted1-like homeobox gene.
AAC32262.1	AF063307	Pisum sativum	Knox class 1 protein. Hop1.
BAA03959.1	D16507	Oryza sativa	homeobox protein. OSH1.
AAG27464.1	AF308454	Medicago truncatula	knotted class I homeodomain KNOX.
AAD00691.1	U90091	Picea mariana	homeobox transcription factor SKN1. knotted1-like homeobox gene.
AAC32817.1	AF050180	Oryza sativa	transcription factor. KNOX class homeodomain protein. Oskn2.
BAA79226.1	AB028885	Oryza sativa	knotted1-type homeobox protein OSH71. OSH71.
BAA79224.1	AB028883	Oryza sativa	knotted1-type homeobox protein OSH6. OSH6.
BAA77818.1	AB007624	Oryza sativa	HOS9. homeobox gene.
BAB19772.1	AP002881	Oryza sativa	putative knotted1-type homeobox protein. P0035H10.13.
AAF23753.2	AF193813	Brassica oleracea	shoot meristemless. Stm. homeodomain protein.
AAD00251.1	U76407	Lycopersicon esculentum	knotted 2 protein. TKn2. homeodomain protein.
CAA96510.1	Z71978	Malus x domestica	kn1-like protein.
BAA31688.1	AB016071	Oryza sativa	OSH15. homeobox gene.
BAA77817.1	AB007623	Oryza sativa	HOS3. homeobox gene.
BAB18582.1	AB043954	Ceratopteris richardii	CRKNOX1. crknox1. knotted1-like homeodomain protein.
BAA76903.1	AB025713	Nicotiana tabacum	homeobox 9. NTH9.

AAD00252.1 U76408 *Lycopersicon esculentum*
knotted 3 protein. TKn3. homeodomain protein.

BAB18584.1 AB043956 *Ceratopteris richardii*
CRKNOX2. crknox2. knotted1-like homeodomain protein.

CAA96511.1 Z71979 *Malus x domestica*
kn1-like protein.

AAA20882.1 L13663 *Glycine max*
SBH1. Sbh1. soybean homeobox-containing gene.

CAB88029.1 AJ276389 *Dendrobium grex Madame Thong-In*
transcription factor. knotted1-like homeobox protein.

SEQ ID NO: 762

AAB65776.1 U97521 *Vitis vinifera*
class IV endochitinase. VvChi4A.

AAB65777.1 U97522 *Vitis vinifera*
class IV endochitinase. VvChi4B.

CAA53626.1 X76041 *Triticum aestivum*
endochitinase. CHI.

AAG53609.1 AF280437 *Secale cereale*
31.7 kDa class I endochitinase-antifreeze protein precursor. cht9.

BAA03750.1 D16222 *Oryza sativa*
endochitinase. Cht-2.

AAA32986.1 M95835 *Brassica napus*
endochitinase. Ch25.

BAA03749.1 D16221 *Oryza sativa*
endochitinase. Cht-1.

AAB01895.1 U48687 *Castanea sativa*
endochitinase.

SEQ ID NO: 763

AAA34065.1 M94135 *Nicotiana tabacum*
chloroplast carbonic anhydrase.

AAA34057.1 L19255 *Nicotiana tabacum*
carbonic anhydrase.

AAB65822.1 U55838 *Populus tremula x Populus tremuloides*
carbonic anhydrase. CA1b. EC 4.2.1.1.

AAC49785.1 U55837 *Populus tremula x Populus tremuloides*
carbonic anhydrase. CA1a. EC 4.2.1.1.

AAA34026.1 M27295 *Spinacia oleracea*
carbonic anhydrase precursor.

AAA34027.1 J05403 *Spinacia oleracea*
carbonic anhydrase (EC 4.2.1.1).

AAA86993.1 U19738 *Flaveria linearis*
reversible hydration of carbon dioxide. carbonic anhydrase 1.

AAA86942.1	U08402	Flaveria brownii	carbonic anhydrase.
AAA86992.1	U19737	Flaveria pringlei	reversible hydration of carbon dioxide. carbonic anhydrase.
AAA86939.1	U08398	Flaveria bidentis	carbonic anhydrase.
AAD27876.2	AF139464	Vigna radiata	carbonic anhydrase. CipCa1.
AAA33652.1	M63627	Pisum sativum	carbonic anhydrase.
AAD29050.1	AF132855	Gossypium hirsutum	interconversion of CO ₂ and HCO ₃ ⁻ . carbonic anhydrase isoform 2. CA2. zinc metalloenzyme; carbonate dehydratase.
AAD29049.1	AF132854	Gossypium hirsutum	interconversion of CO ₂ and HCO ₃ ⁻ . carbonic anhydrase isoform 1. CA1. zinc metalloenzyme; carbonate dehydratase.
AAA86994.1	U19740	Flaveria linearis	reversible hydration of carbon dioxide. carbonic anhydrase 2.
CAB43571.1	AJ239132	Glycine max	hydration of carbon dioxide. carbonic anhydrase. ca1.
CAA63712.1	X93312	Medicago sativa	Carbonic anhydrase. ca1.
AAA86945.1	U08403	Zea mays	carbonic anhydrase.
AAA86944.1	U08401	Zea mays	carbonic anhydrase.
AAC41656.1	L36959	Hordeum vulgare	carbonic anhydrase. putative.
AAA86943.1	U08404	Oryza sativa	carbonic anhydrase. nuclear encoded, localized to chloroplast.
AAD56038.1	AF182806	Oryza sativa	carbonic anhydrase 3. ca3.
BAA31953.1	AB016283	Oryza sativa	carbonic anhydrase.
AAA69027.1	U19739	Urochloa panicoides	reversible hydration of carbon dioxide. carbonic anhydrase 2.
AAA69028.1	U19741	Urochloa panicoides	reversible hydration of carbon dioxide. carbonic anhydrase 1.
BAA95793.1	AB009887	Nicotiana tabacum	carbonic anhydrase. carbonic anhydrase.
AAF78507.1	AF195204	Pyrus pyrifolia	carbonic anhydrase isoform 1. CA1.

AAC33484.1 U49976 *Coccomyxa* sp. PA
beta-type carbonic anhydrase beta-CA1.

AAA18560.1 M95073 *Zea mays*
putative. silimar to carbonic anhydrases.

AAB19184.1 U41190 *Chlamydomonas reinhardtii*
carbonic anhydrase precursor. beta-CA2.

AAB19183.1 U41189 *Chlamydomonas reinhardtii*
carbonic anhydrase precursor. beta-CA1.

AAC49887.1 U80804 *Chlamydomonas reinhardtii*
beta-carbonic anhydrase. ca1. beta-CA1.

AAC49888.1 U80805 *Chlamydomonas reinhardtii*
beta-carbonic anhydrase. ca2. beta-CA2.

SEQ ID NO: 764

AAC06027.1 AF052058 *Vigna unguiculata*
iron storage and mobilization in plants. ferritin subunit cowpea2 precursor.

AAD50644.1 AF133814 *Solanum tuberosum*
ferritin 1. F1.

AAB53099.1 U68217 *Brassica napus*
iron binding protein. ferritin. LSC30.

AAA33959.1 M64337 *Glycine max*
ferritin light chain. ferritin.

AAA34016.1 M72894 *Glycine max*
ferritin light chain. SOF-H2.

CAA58146.1 X83076 *Zea mays*
ferritin. Fer1.

AAB18928.1 U31648 *Glycine max*
iron storage protein. ferritin.

CAA65771.1 X97059 *Medicago sativa*
iron storage. ferritin. FER. abscissic acid regulated.

CAA43663.1 X61391 *Zea mays*
ferritin.

CAA58147.1 X83077 *Zea mays*
ferritin. Fer2.

AAC06026.1 AF052057 *Vigna unguiculata*
iron storage and mobilization in plants. ferritin subunit cowpea3 precursor.

CAA43664.1 X61392 *Zea mays*
ferritin.

CAA51786.1 X73369 *Pisum sativum*
ferritin.

CAA45763.1 X64417 *Pisum sativum*
ferritin-precursor.

CAA41213.1	X58274	Phaseolus vulgaris ferritin. pfe.
AAA33958.1	M58336	Glycine max ferritin light chain. SOF-5L.
CAB42587.1	AJ238628	Chlorella protothecoides putative ferritin. dee188.
BAB17852.1	AB042612	Nicotiana tabacum ferritin 1. tob-fer-1. putative.
AAC15241.1	AF028072	Pinus taeda ferritin.
CAA47983.1	X67755	Vigna unguiculata ferritin 2. pfe2.
CAA47982.1	X67754	Vigna unguiculata ferritin 1. pfe1.
CAA47984.1	X67756	Vigna unguiculata ferritin 5. pfe5.
AAC12282.1	AF052511	Glycine max iron storage and mobilization. ferritin 2. soybean 2; cowpea 2 homolog.
AAC12281.1	AF052513	Glycine max iron storage and mobilization. ferritin 1. soybean 1; cowpea 1 homolog.
SEQ ID NO: 765		
AAC36697.1	AF075579	Mesembryanthemum crystallinum protein phosphatase-2C. PP2C.
CAC10358.1	AJ277086	Nicotiana tabacum protein phosphatase 2C. PP2C1.
CAB90633.1	AJ277743	Fagus sylvatica protein phpsphatase 2C (PP2C). pp2C1. ABA-induced protein.
AAD17804.1	AF092431	Lotus japonicus nodule-enhanced protein phosphatase type 2C. NPP2C1.
CAC10359.1	AJ277087	Nicotiana tabacum protein phosphatase 2C. PP2C2.
CAC09575.1	AJ298987	Fagus sylvatica protein phosphatase 2C (PP2C). pp2Cf1.
CAA72341.1	Y11607	Medicago sativa protein phosphatase 2C. MP2C.
CAB61839.1	AJ242803	Sporobolus stapfianus putative serine/threonine phosphatase type 2c.
AAD17805.1	AF092432	Lotus japonicus protein phosphatase type 2C. PP2C2.
AAG43835.1	AF213455	Zea mays protein phosphatase type-2C. pp2c-1. PP2C-1.

AAG46118.1	AC073166	Oryza sativa	putative protein phosphatase-2C. OSJNBb0064P21.12. tRNA-Lys.
AAG13599.1	AC051633	Oryza sativa	putative protein phosphatase-2C. OSJNBb0015I11.26.
AAC36698.1	AF075580	Mesembryanthemum crystallinum	protein phosphatase-2C. PP2C.
BAB12036.1	AP002820	Oryza sativa	putative protein phosphatase. P0702D12.18.
AAC36700.1	AF075582	Mesembryanthemum crystallinum	protein phosphatase-2C. PP2C.
AAC36699.1	AF075581	Mesembryanthemum crystallinum	protein phosphatase-2C. PP2C.
AAK20060.1	AC025783	Oryza sativa	putative protein phosphatase 2C. OSJNBa0001O14.1.
AAD11430.1	AF097667	Mesembryanthemum crystallinum	protein phosphatase 2C homolog. PP2C.
CAB90634.1	AJ277744	Fagus sylvatica	protein phosphatase 2C (PP2C). pp2C2. ABA and calcium induced protein.
AAC35951.1	AF079355	Mesembryanthemum crystallinum	protein phosphatase-2c. PP2C.
AAF19804.1	AF180355	Brassica oleracea	ABI1 protein. ABI1. similar to Arabidopsis thaliana ABI1.
AAB93832.1	U81960	Zea mays	kinase interaction domain mediates phosphorylation-dependent binding to a subset of active receptor-like protein kinases; type 2C protein phosphatase. kinase associated protein phosphatase. KAPP.
AAC26828.1	AF075603	Oryza sativa	kinase interaction domain mediates phosphorylation-dependent binding to a subset of active receptor-like protein kinases. kinase associated protein phosphatase. kapp. type 2C protein phosphatase.
CAC09576.1	AJ298988	Fagus sylvatica	protein phosphatase 2C (PP2C). pp2Cf2.
SEQ ID NO: 766			
AAG08959.1	AF122051	Solanum tuberosum	tuber-specific and sucrose-responsive element binding factor. TSF. R2R3 MYB class transcription factor.
AAG08960.1	AF122052	Solanum tuberosum	tuber-specific and sucrose-responsive element binding factor. TSF. R2R3 MYB class transcription factor.
AAG08961.1	AF122053	Solanum tuberosum	tuber-specific and sucrose-responsive element binding factor. TSF. R2R3 MYB class transcription factor.

BAA88169.1	AP000836	Oryza sativa	Similar to putative transcription factor (AF062890).
BAA88205.1	AP000837	Oryza sativa	Similar to putative transcription factor (AF062890).
AAF34434.1	AF172282	Oryza sativa	myb-like protein. DUPR11.29.
AAF78890.1	AF189788	Hordeum vulgare	putative c-myb-like transcription factor. MYB3R-1. HvMYB3R-1.
AAF78889.1	AF189787	Hordeum vulgare	putative c-myb-like transcription factor. MYB3R-1. HvMYB3R-1.
AAF67053.1	AF190304	Adiantum raddianum	c-myb-like transcription factor. MYB3R-1. contains three MYB repeats.
AAF67052.1	AF190303	Adiantum raddianum	c-myb-like transcription factor. MYB3R-1. contains three MYB repeats.
AAF78888.1	AF189786	Physcomitrella patens	putative c-myb-like transcription factor. MYB3R-1. PpMYB3R-1.
AAF78887.1	AF189785	Physcomitrella patens	putative c-myb-like transcription factor. MYB3R-1. PpMYB3R-1.
AAF43043.1	AF236059	Papaver rhoeas	putative Myb-related domain. pmr.
BAA94769.1	AP001859	Oryza sativa	Similar to Arabidopsis thaliana chromosome 4, BAC clone F4D11; putative myb-protein. (AL022537).
AAF67050.1	AF190301	Secale cereale	c-myb-like transcription factor. MYB3R-1. contains three MYB repeats.
AAF67051.1	AF190302	Secale cereale	c-myb-like transcription factor. MYB3R-1. contains three MYB repeats.
CAA78388.1	Z13998	Petunia x hybrida	DNA-binding protein; transcriptional activator. protein 3. myb.Ph3. related to animal myb proto-oncoproteins.
BAB39987.1	AP003020	Oryza sativa	putative transcription factor (myb). P0498A12.16. contains ESTs AU097474(S5087),D40175(S1959).
BAB39972.1	AP003018	Oryza sativa	putative transcription factor (myb). OSJNBa0004B13.27. contains ESTs AU097474(S5087),D40175(S1959).
CAA72218.1	Y11415	Oryza sativa	myb.
BAA81731.1	AB029160	Glycine max	GmMYB29A1.
BAA81730.1	AB029159	Glycine max	GmMYB29A1.

CAA72217.1	Y11414	Oryza sativa	myb.
BAA81736.1	AB029165	Glycine max	GmMYB29B2.
BAB12688.1	AP002746	Oryza sativa	putative MYB family transcription factor. P0671B11.3. contains ESTs AU082307(E0784),C72014(E0784).
BAA99440.1	AP002743	Oryza sativa	putative MYB family transcription factor. P0710E05.27. contains ESTs AU082307(E0784),C72014(E0784).
AAB41101.1	U72762	Nicotiana tabacum	transcription factor Myb1. myb1. TMV-inducible Myb homolog; contains helix-turn-helix motif; contains redox-sensitive cysteine.
BAA88223.1	AB028651	Nicotiana tabacum	myb-related transcription factor LBM3. lbm3.
BAA23340.1	D88620	Oryza sativa	transfactor. OSMYB4. Osmbyb4.
BAA93038.1	AP001552	Oryza sativa	EST AU082058(C12976) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana putative transcription factor (AF062916).
AAA33067.1	L04497	Gossypium hirsutum	MYB A; putative.
BAA81733.2	AB029162	Glycine max	GmMYB29A2.
BAA88222.1	AB028650	Nicotiana tabacum	myb-related transcription factor LBM2. lbm2.
CAB43399.1	AJ006292	Antirrhinum majus	Myb-related transcription factor mixta-like 1. mybm11.
BAA81732.1	AB029161	Glycine max	GmMYB29A2.
AAG28525.1	AF198498	Nicotiana tabacum	anther-specific myb-related protein 2. mybAS2. NtMYBAS2; contains tandem R2, R3 myb domains similar to c-myb family.
CAA50226.1	X70881	Hordeum vulgare	MybHv33. myb3.
CAA50223.1	X70878	Hordeum vulgare	MybHv33. myb3.
CAA78387.1	Z13997	Petunia x hybrida	DNA-binding protein, transcriptional activator. protein 2. myb.Ph2. related to animal myb proto-oncoproteins.
CAA67000.1	X98355	Oryza sativa	activator of alpha-amylase gene promoter. transcription factor GAMyb. Gam1. Myb-like; expression is regulated by gibberellin.

AAK19616.1	AF336283	Gossypium hirsutum	GHMYB25. ghmyb25. similar to myb; contains an unspliced intron.
AAG28526.1	AF198499	Nicotiana tabacum	anther-specific myb-related protein 1. mybAS1. NtMYBAS1; contains N-terminal R2, R3 myb domain repeats similar to c-myb.
CAA78386.1	Z13996	Petunia x hybrida	DNA binding protein; transcriptional activator. protein 1. myb.Ph3. Product related to animal myb proto-oncoproteins. Sequence from nucleotide 992 is not included in clone cPF1 and has been obtained by PCR amplification of cDNA.
CAA66952.1	X98308	Lycopersicon esculentum	THM18. myb-related transcription factor.
BAA23341.1	D88621	Oryza sativa	transfactor. OSMYB5. Osmyb5.
CAA50221.1	X70876	Hordeum vulgare	MybHv5. myb2.
AAK19611.1	AF336278	Gossypium hirsutum	BNLGHi233. bnlghi6233. similar to myb.
AAC04716.1	AF034130	Gossypium hirsutum	putative MYB-like transcription factor. MYB-like DNA-binding domain protein. Cmy-D. similar to MYB A encoded by GenBank Accession Number L04497.
CAA61021.1	X87690	Hordeum vulgare	transcriptional activator of alpha-amylase gene promoter. GAMyb protein. Gam1.
AAG22863.1	AY008692	Hordeum vulgare	transcription factor GAMyb. Gamyb.
SEQ ID NO: 767			
CAB08111.1	Z94180	Lycopersicon esculentum	branched chain alpha-keto acid dehydrogenase E1-alpha subunit.
CAA81558.1	Z26949	Solanum tuberosum	subunit of the mitochondrial pyruvate dehydrogenase complex. E1 alpha subunit of pyruvate dehydrogenase precursor.
AAC72195.1	AF069911	Zea mays	pyruvate dehydrogenase E1 alpha subunit.
AAG43499.1	AF209924	Lycopersicon esculentum	pyruvate dehydrogenase.
AAA97411.1	U51918	Pisum sativum	pyruvate dehydrogenase E1 alpha subunit.
CAA10992.1	AJ222787	Hordeum vulgare	alpha-keto acid dehydrogenase-like protein. homology to branched chain alpha-keto acid dehydrogenase E1-alpha subunit.
SEQ ID NO: 768			
AAF64450.1	AF239928	Euphorbia esula	glutathione S-transferase. similar to auxin-inducible GST.

AAG16758.1 AY007560 *Lycopersicon esculentum*
putative glutathione S-transferase T3.

AAG34803.1 AF243368 *Glycine max*
glutathione S-transferase GST 13.

AAG16756.1 AY007558 *Lycopersicon esculentum*
putative glutathione S-transferase T1.

AAG34796.1 AF243361 *Glycine max*
glutathione S-transferase GST 6.

AAG34809.1 AF243374 *Glycine max*
glutathione S-transferase GST 19.

AAG34797.1 AF243362 *Glycine max*
glutathione S-transferase GST 7.

AAG34807.1 AF243372 *Glycine max*
glutathione S-transferase GST 17.

AAG34798.1 AF243363 *Glycine max*
glutathione S-transferase GST 8.

AAG34804.1 AF243369 *Glycine max*
glutathione S-transferase GST 14.

AAG16759.1 AY007561 *Lycopersicon esculentum*
putative glutathione S-transferase T4.

AAG34801.1 AF243366 *Glycine max*
glutathione S-transferase GST 11.

AAG34810.1 AF243375 *Glycine max*
glutathione S-transferase GST 20.

AAG16757.1 AY007559 *Lycopersicon esculentum*
putative glutathione S-transferase T2.

AAC18566.1 AF048978 *Glycine max*
2,4-D inducible glutathione S-transferase. GSTa.

AAG34808.1 AF243373 *Glycine max*
glutathione S-transferase GST 18.

AAG34800.1 AF243365 *Glycine max*
glutathione S-transferase GST 10.

CAA71784.1 Y10820 *Glycine max*
glutathione transferase.

AAG34844.1 AF244701 *Zea mays*
glutathione S-transferase GST 36.

AAG32472.1 AF309379 *Oryza sativa* subsp. *japonica*
putative glutathione S-transferase OsGSTU3.

AAA68430.1 J03679 *Solanum tuberosum*
glutathione S-transferase. *gst1*. previously called pathogenesis-related protein; *prp1-1*.

CAA04391.1 AJ000923 *Carica papaya*
glutathione transferase. PGST1.

AAG34831.1	AF244688	Zea mays glutathione S-transferase GST 23.
CAA09187.1	AJ010448	Alopecurus myosuroides glutathione transferase. GST1a.
CAA09188.1	AJ010449	Alopecurus myosuroides glutathione transferase. GST1b.
AAG34802.1	AF243367	Glycine max glutathione S-transferase GST 12.
AAG34805.1	AF243370	Glycine max glutathione S-transferase GST 15.
AAG34832.1	AF244689	Zea mays glutathione S-transferase GST 24.
AAG34837.1	AF244694	Zea mays glutathione S-transferase GST 29.
AAG34836.1	AF244693	Zea mays glutathione S-transferase GST 28.
AAG32471.1	AF309378	Oryza sativa subsp. japonica putative glutathione S-transferase OsGSTU4.
AAG34849.1	AF244706	Zea mays glutathione S-transferase GST 41.
CAC24549.1	AJ296343	Cichorium intybus x Cichorium endivia glutathione S-transferase. chi-GST1. auxin-induced GST.
AAC32118.1	AF051214	Picea mariana probable glutathione S-transferase. Sb18. similar to Nicotiana tabacum probable glutathione S-transferase encoded by GenBank Accession Number X56266.
AAG34795.1	AF243360	Glycine max glutathione S-transferase GST 5.
AAG34841.1	AF244698	Zea mays glutathione S-transferase GST 33.
AAF29773.1	AF159229	Gossypium hirsutum glutathione S-transferase. GST.
SEQ ID NO: 769		
AAG34797.1	AF243362	Glycine max glutathione S-transferase GST 7.
AAG34798.1	AF243363	Glycine max glutathione S-transferase GST 8.
AAG34803.1	AF243368	Glycine max glutathione S-transferase GST 13.
AAG16758.1	AY007560	Lycopersicon esculentum putative glutathione S-transferase T3.
AAF64450.1	AF239928	Euphorbia esula glutathione S-transferase. similar to auxin-inducible GST.

AAG34801.1 AF243366 Glycine max
glutathione S-transferase GST 11.

AAG34804.1 AF243369 Glycine max
glutathione S-transferase GST 14.

AAG34796.1 AF243361 Glycine max
glutathione S-transferase GST 6.

AAG34809.1 AF243374 Glycine max
glutathione S-transferase GST 19.

AAG16759.1 AY007561 Lycopersicon esculentum
putative glutathione S-transferase T4.

AAG16757.1 AY007559 Lycopersicon esculentum
putative glutathione S-transferase T2.

AAG16756.1 AY007558 Lycopersicon esculentum
putative glutathione S-transferase T1.

AAG34807.1 AF243372 Glycine max
glutathione S-transferase GST 17.

AAG34810.1 AF243375 Glycine max
glutathione S-transferase GST 20.

AAG34844.1 AF244701 Zea mays
glutathione S-transferase GST 36.

AAG34831.1 AF244688 Zea mays
glutathione S-transferase GST 23.

AAC18566.1 AF048978 Glycine max
2,4-D inducible glutathione S-transferase. GSTa.

AAG34832.1 AF244689 Zea mays
glutathione S-transferase GST 24.

AAG34808.1 AF243373 Glycine max
glutathione S-transferase GST 18.

AAG34837.1 AF244694 Zea mays
glutathione S-transferase GST 29.

AAG34800.1 AF243365 Glycine max
glutathione S-transferase GST 10.

AAG34836.1 AF244693 Zea mays
glutathione S-transferase GST 28.

CAA04391.1 AJ000923 Carica papaya
glutathione transferase. PGST1.

CAA71784.1 Y10820 Glycine max
glutathione transferase.

AAG34849.1 AF244706 Zea mays
glutathione S-transferase GST 41.

AAA68430.1 J03679 Solanum tuberosum
glutathione S-transferase. gst1. previously called pathogenesis-related protein; prp1-1.

AAG34802.1	AF243367	Glycine max glutathione S-transferase GST 12.
CAC24549.1	AJ296343	Cichorium intybus x Cichorium endivia glutathione S-transferase. chi-GST1. auxin-induced GST.
CAA09187.1	AJ010448	Alopecurus myosuroides glutathione transferase. GST1a.
AAF22518.1	AF118925	Papaver somniferum glutathione S-transferase 2. GST2.
AAG32471.1	AF309378	Oryza sativa subsp. japonica putative glutathione S-transferase OsGSTU4.
CAA09188.1	AJ010449	Alopecurus myosuroides glutathione transferase. GST1b.
AAF22517.1	AF118924	Papaver somniferum glutathione S-transferase 1. GST1.
AAF22647.1	AF193439	Lycopersicon esculentum glutathione S-transferase/peroxidase. BI-GST/GPX.
AAG32473.1	AF309380	Oryza sativa subsp. japonica putative glutathione S-transferase OsGSTU2.
AAG32472.1	AF309379	Oryza sativa subsp. japonica putative glutathione S-transferase OsGSTU3.
SEQ ID NO: 771		
AAG46118.1	AC073166	Oryza sativa putative protein phosphatase-2C. OSJNBb0064P21.12. tRNA-Lys.
AAG13599.1	AC051633	Oryza sativa putative protein phosphatase-2C. OSJNBb0015I11.26.
BAB12036.1	AP002820	Oryza sativa putative protein phosphatase. P0702D12.18.
AAC36698.1	AF075580	Mesembryanthemum crystallinum protein phosphatase-2C. PP2C.
CAA72341.1	Y11607	Medicago sativa protein phosphatase 2C. MP2C.
AAG43835.1	AF213455	Zea mays protein phosphatase type-2C. pp2c-1. PP2C-1.
CAB61839.1	AJ242803	Sporobolus stapfianus putative serine/threonine phosphatase type 2c.
AAD17804.1	AF092431	Lotus japonicus nodule-enhanced protein phosphatase type 2C. NPP2C1.
AAD17805.1	AF092432	Lotus japonicus protein phosphatase type 2C. PP2C2.
AAC36697.1	AF075579	Mesembryanthemum crystallinum protein phosphatase-2C. PP2C.

CAB90633.1	AJ277743	Fagus sylvatica	protein phpsphatase 2C (PP2C). pp2C1. ABA-induced protein.
CAC10358.1	AJ277086	Nicotiana tabacum	protein phosphatase 2C. PP2C1.
CAC10359.1	AJ277087	Nicotiana tabacum	protein phosphatase 2C. PP2C2.
AAC36700.1	AF075582	Mesembryanthemum crystallinum	protein phosphatase-2C. PP2C.
CAC09575.1	AJ298987	Fagus sylvatica	protein phosphatase 2C (PP2C). pp2Cf1.
AAK20060.1	AC025783	Oryza sativa	putative protein phosphatase 2C. OSJNBa0001O14.1.
CAB90634.1	AJ277744	Fagus sylvatica	protein phosphatase 2C (PP2C). pp2C2. ABA and calcium induced protein.
AAC35951.1	AF079355	Mesembryanthemum crystallinum	protein phosphatase-2c. PP2C.
AAD11430.1	AF097667	Mesembryanthemum crystallinum	protein phosphatase 2C homolog. PP2C.
AAB93832.1	U81960	Zea mays	kinase interaction domain mediates phosphorylation-dependent binding to a subset of active receptor-like protein kinases; type 2C protein phosphatase. kinase associated protein phosphatase. KAPP.
AAC26828.1	AF075603	Oryza sativa	kinase interaction domain mediates phosphorylation-dependent binding to a subset of active receptor-like protein kinases. kinase associated protein phosphatase. kapp. type 2C protein phosphatase.
AAC36699.1	AF075581	Mesembryanthemum crystallinum	protein phosphatase-2C. PP2C.
CAC09576.1	AJ298988	Fagus sylvatica	protein phosphatase 2C (PP2C). pp2Cf2.
SEQ ID NO: 777			
AAD21872.1	AF078082	Phaseolus vulgaris	receptor-like protein kinase homolog RK20-1.
AAB93834.1	U82481	Zea mays	KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
CAA74661.1	Y14285	Brassica oleracea	SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.
AAD52097.1	AF088885	Nicotiana tabacum	receptor-like kinase CHRK1. Chrkl.
CAA73134.1	Y12531	Brassica oleracea	serine/threonine kinase. BRLK.

CAB41879.1	Y18260	Brassica oleracea	SRK15 protein. SRK15. receptor-like kinase.
CAB41878.1	Y18259	Brassica oleracea	SRK5 protein. SRK5. receptor-like kinase.
AAA33008.1	M97667	Brassica napus	serine/threonine kinase receptor.
CAB89179.1	AJ245479	Brassica napus subsp. napus	ser /thr kinase. S-locus receptor kinase. srk.
CAA67145.1	X98520	Brassica oleracea	receptor-like kinase. SFR2.
AAA33000.1	M76647	Brassica oleracea	receptor protein kinase. SKR6.
CAA73133.1	Y12530	Brassica oleracea	serine /threonine kinase. ARLK.
AAA62232.1	U00443	Brassica napus	S-receptor kinase. protein contains an immunoglobulin-like domain.
AAC23542.1	U20948	Ipomoea trifida	receptor protein kinase. IRK1.
CAA74662.1	Y14286	Brassica oleracea	SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
BAA92837.1	AB032474	Brassica oleracea	S60 S-locus receptor kinase. SRK60.
BAA07577.2	D38564	Brassica rapa	receptor protein kinase SRK12.
BAA23676.1	AB000970	Brassica rapa	receptor kinase 1. BcRK1.
CAA79355.1	Z18921	Brassica oleracea	S-receptor kinase-like protein.
BAB21001.1	AB054061	Brassica rapa	S locus receptor kinase. SRK22.
BAA21132.1	D88193	Brassica rapa	S-receptor kinase. SRK9 (B.c).
BAA06285.1	D30049	Brassica rapa	S-receptor kinase SRK9.
BAA92836.1	AB032473	Brassica oleracea	S18 S-locus receptor kinase. SRK18.
BAA07576.1	D38563	Brassica rapa	receptor protein kinase SRK8.
BAB18292.1	AP002860	Oryza sativa	putative receptor-like protein kinase. P0409B08.19.
AAK21965.1	AY028699	Brassica napus	receptor protein kinase PERK1.

BAA92954.1	AP001551	Oryza sativa	Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).
BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.
BAB39435.1	AP003338	Oryza sativa	putative receptor kinase. OJ1212_B09.2.
BAB07904.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.12.
BAA94518.1	AP001800	Oryza sativa	Similar to Arabidopsis thaliana chromosome 2 section 111 of 255; putative receptor-like protein kinase (AC002392).
AAG16628.1	AY007545	Brassica napus	protein serine/threonine kinase BNK1.
BAB39409.1	AP002901	Oryza sativa	putative protein kinase. P0456F08.9. contains EST C23560(R0290).
BAB16871.1	AP002537	Oryza sativa	putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
AAF91324.1	AF244890	Glycine max	receptor-like protein kinase 3. RLK3. GmRLK3.
BAA82556.1	AB030083	Populus nigra	lectin-like protein kinase. PnLPK.
AAF91323.1	AF244889	Glycine max	receptor-like protein kinase 2. RLK2. GmRLK2.
AAF91322.1	AF244888	Glycine max	receptor-like protein kinase 1. RLK1. GmRLK1.
SEQ ID NO: 779			
AAK31284.1	AC079890	Oryza sativa	putative quinone oxidoreductase. OSJNBb0089A17.10.
BAA78050.1	AB027757	Cicer arietinum	NADPH oxidoreductase homolog.
BAA83082.1	AB030704	Lithospermum erythrorhizon	LEDI-4 protein. LEDI-4. preferentially expressed in darkness; putative NADPH quinone oxidoreductase; similar to zeta-crystallin.
AAG53944.1	AF304461	Triphysaria versicolor	quinone-oxidoreductase QR1. TvQR1.
SEQ ID NO: 780			
AAK17067.1	AF254558	Oryza sativa	NAC6. NAC6.

BAA89800.1 AB028185 *Oryza sativa*
OsNAC6 protein. OsNAC6.

BAA89799.1 AB028184 *Oryza sativa*
OsNAC5 protein. OsNAC5.

BAA89798.1 AB028183 *Oryza sativa*
OsNAC4 protein. OsNAC4.

BAA89797.1 AB028182 *Oryza sativa*
OsNAC3 protein. OsNAC3.

BAA89801.1 AB028186 *Oryza sativa*
OsNAC7 protein. OsNAC7.

AAF68626.1 AF254124 *Medicago truncatula*
NAC1. NAC1. NAC domain containing protein.

BAA89802.1 AB028187 *Oryza sativa*
OsNAC8 protein. OsNAC8.

BAA78417.1 AB021178 *Nicotiana tabacum*
NAC-domain protein. TERN. elicitor-responsive gene.

SEQ ID NO: 783

CAA54390.1 X77134 *Brassica napus*
acyl-CoA binding protein.

CAA70200.1 Y08996 *Ricinus communis*
acyl-CoA-binding protein.

CAB56693.1 AJ249833 *Digitalis lanata*
binds medium- and long-chain acyl-coa esters. Acyl-CoA binding protein (ACBP). acbp3.

CAB56694.1 AJ249834 *Digitalis lanata*
binds medium- and long-chain acyl-coa esters. Acyl-CoA binding protein (ACBP). acbp4.

AAB67736.1 U35015 *Gossypium hirsutum*
acyl-CoA-binding protein.

AAB86851.1 AF031541 *Fritillaria agrestis*
acyl-CoA-binding protein. acabp.

SEQ ID NO: 784

CAA58994.1 X84208 *Sinapis alba*
trypsin inhibitor 2. mti-2.

CAA76116.1 Y16190 *Sinapis alba*
trypsin inhibitor 2. mti-2.

SEQ ID NO: 785

AAF66242.1 AF243180 *Lycopersicon esculentum*
dicyanin. binuclear blue copper protein; contains two stellacyanins linked together.

AAC32421.1	U65511	Cucumis sativus	putative oxygen activation and/or lignin formation. stellacyanin. member of a strictly plant-specific family of mononuclear blue copper proteins known as phytoeyanins, which are further classified into three distinct subfamilies: Uclacyanins, Stellacyanins, and Plantacyanins; member of the subfamily of Stellacyanins; similar to Rhus vernicifera stellacyanin: SwissProt Accession Number P00302; similar to umecyanin: SwissProt Accession Number P42849; similar to mavicyanin; SwissProt Accession Number P80728; similar to BCB encoded by GenBank Accession Number Z15058; similar to F18A8.9, encoded by GenBank Accession Number AC003105; similar to F7F1.27 encoded by GenBank Accession Number AC004669; similar to F9D12.16 encoded by GenBank Accession Number AF077407; glycoprotein.
CAA80963.1	Z25471	Pisum sativum	blue copper protein.
AAD10251.1	AF031195	Triticum aestivum	blue copper-binding protein homolog. S85.
AAC64163.1	AF093537	Zea mays	blue copper protein. similar to pea blue copper protein in GenBank Accession Number Z25471.
CAA10134.1	AJ012693	Cicer arietinum	basic blue copper protein.
AAF66243.1	AF243181	Lycopersicon esculentum	plantacyanin. naturally occurring cupredoxin with a Val residue in the position of the axial ligand Met; member of the plantacyanin subfamily of a strictly plant-specific family of mononuclear blue copper proteins known as phytoeyanins.
CAB65280.1	AJ248323	Medicago sativa subsp. x varia	basic blue protein. babl.
AAC32448.1	U76296	Spinacia oleracea	plantacyanin. member of a strictly plant-specific family of mononuclear blue copper proteins known as phytoeyanins, which are further classified into three distinct subfamilies: Uclacyanins, Stellacyanins, and Plantacyanins; member of the subfamily of Plantacyanins; non-glycosylated.
SEQ ID NO: 793			
BAA81862.1	AB026295	Oryza sativa	Similar to leucoanthocyanidin dioxygenase.(AI440611).
AAB39995.1	U82432	Dianthus caryophyllus	anthocyanidin synthase. allele: S; 2-oxoglutarat-dependent dioxygenase.
BAA36554.1	AB011796	Citrus unshiu	flavonol synthase. CitFLS.
AAD56580.1	AF184273	Daucus carota	leucoanthocyanidin dioxygenase 1. LDOX1. 2-oxoglutarate dependent dioxygenase.
AAD56581.1	AF184274	Daucus carota	leucoanthocyanidin dioxygenase 2. LDOX. 2-oxoglutarate dependent dioxygenase.
CAA50498.1	X71360	Malus sp.	anthocyanidin hydroxylase. apple equivalent to 'Candi' from Antirrhinum majus.

AAD26205.1	AF117269	Malus x domestica	anthocyanidin synthase. ANS.
AAB82287.1	AF026058	Matthiola incana	anthocyanidin synthase.
CAA80264.1	Z22543	Petunia x hybrida	flavonol synthase.
AAF64168.1	AF240764	Eustoma grandiflorum	flavonol synthase. fls.
BAA20143.1	AB003779	Perilla frutescens	leucoanthocyanidin dioxygenase.
AAB66560.1	AF015885	Callistephus chinensis	anthocyanidin synthase.
BAB21477.1	AB044091	Torenia fournieri	anthocyanidin synthase. 2-oxoglutarate dependent oxygenase.
CAA63092.1	X92178	Solanum tuberosum	flavonol synthase.
AAD26261.1	AF119095	Malus x domestica	flavonol synthase. FLS.
CAA53580.1	X75966	Vitis vinifera	leucoanthocyanidin dioxygenase. LDOX.
BAA75305.1	AB023786	Ipomoea batatas	anthocyanidin synthase. ans I.
AAB84049.1	AF028602	Ipomoea purpurea	anthocyanidin synthase. ANS-FL1.
BAA75306.1	AB023787	Ipomoea batatas	anthocyanidin synthase. ans II.
CAA73094.1	Y12489	Forsythia x intermedia	anthocyanidin synthase.
CAA69252.1	Y07955	Oryza sativa	anthocyanidin synthase. ANS.
SEQ ID NO: 794			
AAD10204.1	AF030260	Vicia sativa	CYP94A1. vagh111. cytochrome P450 fatty acid hydroxylase; Method: conceptual translation with partial peptide sequencing.
AAG33645.1	AF092917	Vicia sativa	cytochrome P450-dependent fatty acid hydroxylase. CYP94A2.
AAG17470.1	AF123609	Triticum aestivum	cytochrome P450.
BAA99523.1	AP002484	Oryza sativa	putative cytochrome P450. P0489A01.14.
AAK31592.1	AY029178	Brassica rapa subsp. pekinensis	cytochrome P450. mf-CYP450. possible relevance to male-sterility.

- BAA99522.1 AP002484 *Oryza sativa*
putative cytochrome P450. P0489A01.13.
- BAA83370.1 AP000391 *Oryza sativa*
ESTs AU056036(S20239), C72753(E2173), AU056035(S20239) correspond to a region of the
predicted gene.; Similar to putative cytochrome P-450 (AC003680).
- CAB41474.1 AJ238402 *Catharanthus roseus*
cytochrome P450. CYP96C1.
- AAB94586.1 AF022457 *Glycine max*
CYP97B2p. CYP97B2. cytochrome P450 monooxygenase.
- AAK20054.1 AC025783 *Oryza sativa*
putative cytochrome P450 monooxygenase. OSJNBa0001O14.16.
- AAK38086.1 AF321862 *Lolium rigidum*
putative cytochrome P450.
- AAK38085.1 AF321861 *Lolium rigidum*
putative cytochrome P450.
- AAB94588.1 AF022459 *Glycine max*
CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.
- CAA89260.1 Z49263 *Pisum sativum*
cytochrome P450.
- AAG09208.1 AF175278 *Pisum sativum*
wound-inducible P450 hydroxylase. CYP82A1.
- AAC49188.2 U29333 *Pisum sativum*
cytochrome P450 monooxygenase. CYP82. new cytochrome P450 family.
- BAB19083.1 AP002744 *Oryza sativa*
putative cytochrome P450. P0006C01.25. contains ESTs
AU081507(C12518), C26520(C12518).
- BAB19104.1 AP002839 *Oryza sativa*
putative cytochrome P450. P0688A04.10. contains ESTs
AU081507(C12518), C26520(C12518).
- AAK38092.1 AF321868 *Lolium rigidum*
putative cytochrome P450.
- CAA04117.1 AJ000478 *Helianthus tuberosus*
fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1l. chimeric sequence (from 5'-
race).
- AAK38091.1 AF321867 *Lolium rigidum*
putative cytochrome P450.
- CAA04116.1 AJ000477 *Helianthus tuberosus*
fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1c.
- BAA22423.1 AB001380 *Glycyrrhiza echinata*
cytochrome P450. CYP93B1.
- CAA71876.1 Y10982 *Glycine max*
putative cytochrome P450.

BAB39252.1	AP002968	Oryza sativa	putative cytochrome P450. P0416G11.1.
AAA33106.1	L10081	Catharanthus roseus	cytochrome P-450 protein. CYP72. putative; CYP72 protein.
AAA17746.1	L19075	Catharanthus roseus	cytochrome P450. CYP72C. putative.
BAA74466.1	AB022733	Glycyrrhiza echinata	cytochrome P450. CYP Ge-51.
BAB19121.1	AP002839	Oryza sativa	putative cytochrome P450. P0688A04.28.
AAA17732.1	L19074	Catharanthus roseus	cytochrome P450. CYP72B.
BAA93634.1	AB025016	Lotus japonicus	cytochrome P450.
AAB05376.3	U35226	Nicotiana plumbaginifolia	putative cytochrome P-450.
AAB61965.1	U48435	Solanum chacoense	putative cytochrome P450.
AAF27282.1	AF122821	Capsicum annuum	cytochrome P450. PepCYP.
CAB50768.1	AJ243804	Cicer arietinum	putative isoflavone synthase. cytochrome P450. cyp93C3.
AAC34853.1	AF082028	Hemerocallis hybrid cultivar	putative cyt P450-containing fatty acid hydroxylase. senescence-associated protein 3. SA3. mRNA accumulates in senescing petals.
CAB43505.1	AJ239051	Cicer arietinum	cytochrome P450. cyp81E2.
BAB21156.1	AP002899	Oryza sativa	putative cytochrome P450. P0456A01.12.
CAA50648.1	X71657	Solanum melongena	P450 hydroxylase.
BAB19112.1	AP002839	Oryza sativa	putative cytochrome P450. P0688A04.18. contains ESTs AU067870(C10320),AU067869(C10320).
BAB19091.1	AP002744	Oryza sativa	putative cytochrome P450. P0006C01.33. contains ESTs AU067870(C10320),AU067869(C10320).
BAA84072.1	AB028152	Torenia hybrida	flavone synthase II. cytochrome P450. TFNS5.
BAA76380.1	AB023636	Glycyrrhiza echinata	cytochrome P450. CYP Ge-8.
CAA72208.1	Y11404	Zea mays	cytochrome p450. cyp71c2.

CAA57423.1 X81829 Zea mays
cytochrome P450. CYP71C2. family CYP71, subfamily CYP71C.

BAB12433.1 AB025030 Coptis japonica
p450.

SEQ ID NO: 798

BAB21205.1 AP002913 Oryza sativa
nucleoid DNA-binding protein cnd41-like protein. P0480E02.11. contains ESTs
AU166073(E31027), AU029516(E31027).

BAA22813.1 D26015 Nicotiana tabacum
aspartic protease activity. CND41, chloroplast nucleoid DNA binding protein. cnd41.

SEQ ID NO: 804

AAD46491.1 AF135014 Zea mays
dihydrolipoamide S-acetyltransferase. pyruvate dehydrogenase complex E2 subunit.

SEQ ID NO: 805

BAA85412.1 AP000615 Oryza sativa
ESTs AU065232(E60855), C23624(S1554), AU078241(E60855) correspond to a region of the
predicted gene.; similar to putative adenylate kinase. (AC005896).

BAA01181.1 D10335 Oryza sativa
adenylate kinase-b. Adk-b.

BAA01180.1 D10334 Oryza sativa
adenylate kinase-a. Adk-a.

BAA94761.1 AB041773 Oryza sativa
adenylate kinase. Adk-a.

AAB68604.1 U82330 Prunus armeniaca
adenylate kinase homolog.

AAF23372.1 AF187063 Oryza sativa
catalyzes the transfer of phosphate from ATP to UMP or CMP to form ADP and UDP or
CDP. UMP/CMP kinase b. ura6.

AAF23371.1 AF187062 Oryza sativa
catalyzes the transfer of phosphate from ATP to UMP or CMP to form ADP and UDP or
CDP. UMP/CMP kinase a. ura6.

AAD41679.1 AF086603 Ceratopteris richardii
adenylate kinase. ADK1.

BAA85443.1 AP000616 Oryza sativa
similar to UMP/CMP kinase (AF000147).

SEQ ID NO: 808

CAA41774.1 X59046 Oryza sativa
sucrose-UDP glucosyltransferase (isoenzyme 2). RSs2.

BAA89049.1 AB029401 Citrus unshiu
sucrose synthase. CitSUS1-2.

AAA34196.1 L19762 Lycopersicon esculentum
sucrose synthase.

BAA88905.1	AB022092	Citrus unshiu
sucrose synthase. CitSUS1.		
AAD28641.1	U73588	Gossypium hirsutum
sucrose synthase.		
CAA49428.1	X69773	Vicia faba
sucrose synthase. VfSucs.		
AAC37346.1	M97551	Vicia faba
cleavage of sucrose. UDP-glucose:D-fructose-2-glucosyltransferase. putative.		
CAA09681.1	AJ011535	Lycopersicon esculentum
sucrose synthase. sus2.		
AAA97572.1	U24088	Solanum tuberosum
sucrose synthase.		
CAA09593.1	AJ011319	Lycopersicon esculentum
sucrose synthase. sus3.		
CAB40794.1	AJ131943	Medicago truncatula
sucrose synthase. sucS1.		
AAC17867.1	AF049487	Medicago sativa
sucrose hydrolysis. sucrose synthase.		
CAB40795.1	AJ131964	Medicago truncatula
sucrose synthase. sucS1.		
CAA65640.1	X96939	Tulipa gesneriana
sucrose-synthase 21.		
AAA97571.1	U24087	Solanum tuberosum
sucrose synthase.		
CAA63122.1	X92378	Alnus glutinosa
sucrose synthase. sus1.		
AAA33514.1	L22296	Zea mays
UDP-glucose:D-fructose 2-glucosyl-transferase. Sus1.		
CAA65639.1	X96938	Tulipa gesneriana
sucrose-synthase 1.		
AAC41682.1	L03366	Oryza sativa
sucrose synthase 3. RSs3.		
CAA75793.1	Y15802	Hordeum vulgare
sucrose synthase 2. Ss2.		
CAA49551.1	X69931	Hordeum vulgare
sucrose synthase. Ss2.		
CAA76056.1	Y16090	Daucus carota
sucrose synthase isoform I. Susy*Dc1.		
CAA53081.1	X75332	Daucus carota
sucrose synthase.		
AAA33515.1	L33244	Zea mays
sucrose synthase 2. Sus1.		

BAB20799.1	AB045710	Pyrus pyrifolia	sucrose synthase 1. PypSUS1.
CAA03935.1	AJ000153	Triticum aestivum	sucrose synthase type 2.
AAC39323.1	AF030231	Glycine max	sucrose synthase. SS. nodulin-100.
BAA01108.1	D10266	Vigna radiata	sucrose synthase. vssl.
CAA09910.1	AJ012080	Pisum sativum	sucrose synthase.
AAC28107.1	AF079851	Pisum sativum	nodule-enhanced sucrose synthase. ness.
CAC32462.1	AJ311496	Pisum sativum	sucrose metabolism. sucrose synthase isoform 3. sus3.
CAA57881.1	X82504	Chenopodium rubrum	sucrose synthase. CSS1.
CAA26229.1	X02382	Zea mays	sucrose synthase.
CAA26247.1	X02400	Zea mays	sucrose synthase.
CAA46017.1	X64770	Oryza sativa	sucrose synthase. RSs1.
CAB38022.1	AJ132000	Craterostigma plantagineum	sucrose metabolism. sucrose synthase. Ss2.
CAA78747.1	Z15028	Oryza sativa	sucrose synthase.
AAF85966.1	AF263384	Saccharum officinarum	sucrose synthase-1.
CAA46701.1	X65871	Hordeum vulgare	sucrose synthase.
CAA04543.1	AJ001117	Triticum aestivum	sucrose synthase type I. Ss1.
BAA88904.1	AB022091	Citrus unshiu	sucrose synthase. CitSUSA.
BAA88981.1	AB025778	Citrus unshiu	sucrose synthase. CitSUSA-2.
CAA04512.1	AJ001071	Pisum sativum	second sucrose synthase.
CAA76057.1	Y16091	Daucus carota	sucrose synthase isoform II. Susy*Dc2.
CAB38021.1	AJ131999	Craterostigma plantagineum	sucrose metabolism. sucrose synthase. Ss1.

CAA57499.1 X81974 Beta vulgaris
sucrose synthase. SBSS1.

CAA47264.1 X66728 Hordeum vulgare
sucrose synthase.

SEQ ID NO: 809

AAB69317.1 AF012861 Petroselinum crispum
plastidic glucose-6-phosphate dehydrogenase. pG6PDH.

AAF87216.1 AF231351 Nicotiana tabacum
plastidic glucose 6-phosphate dehydrogenase. G6PDHP2.

CAA67782.1 X99405 Nicotiana tabacum
glucose-6-phosphate dehydrogenase. G6PD.

CAB52708.1 AJ010712 Solanum tuberosum
glucose-6-phosphate 1-dehydrogenase. g6pd.

CAB52685.1 AJ132346 Dunaliella bioculata
plastidic glucose-6-phosphate dehydrogenase. g6PD.

CAA58775.1 X83923 Solanum tuberosum
glucose-6-phosphate dehydrogenase.

CAA03941.1 AJ000184 Spinacia oleracea
Glucose-6-phosphate dehydrogenase. G6PD.

CAA03939.1 AJ000182 Spinacia oleracea
Glucose-6-phosphate dehydrogenase. G6PD.

CAA04994.1 AJ001772 Nicotiana tabacum
glucose-6-phosphate dehydrogenase. TCG18.

CAA03940.1 AJ000183 Spinacia oleracea
Glucose-6-phosphate dehydrogenase. G6PD.

AAD11426.1 AF097663 Mesembryanthemum crystallinum
cytoplasmic glucose-6-phosphate 1-dehydrogenase. G6PD.

AAB41552.1 U18238 Medicago sativa subsp. sativa
glucose-6-phosphate dehydrogenase.

CAA52442.1 X74421 Solanum tuberosum
glucose-6-phosphate 1-dehydrogenase. g6pdh. homotetramer.

AAB69318.1 AF012862 Petroselinum crispum
cytosolic glucose-6-phosphate dehydrogenase 1. cG6PDH1.

AAB69319.1 AF012863 Petroselinum crispum
cytosolic glucose-6-phosphate dehydrogenase 2. cG6PDH2.

CAA04992.1 AJ001769 Nicotiana tabacum
glucose-6-phosphate dehydrogenase. TCG6.

CAA04993.1 AJ001770 Nicotiana tabacum
glucose-6-phosphate dehydrogenase. TCG9.

BAA97662.1 AB029454 Triticum aestivum
glucose-6-phosphate dehydrogenase. g6pdh.

BAA97663.1 AB029455 *Triticum aestivum*
glucose-6-phosphate dehydrogenase. g6pdh.

BAA97664.1 AB029456 *Triticum aestivum*
glucose-6-phosphate dehydrogenase. g6pdh.

AAG23802.1 AF260736 *Cucurbita pepo*
plastidic glucose-6-phosphate dehydrogenase.

CAB66330.1 AJ279688 *Betula pendula*
glucose-6-phosphate dehydrogenase. g6pd.

BAA82155.1 AB011441 *Triticum aestivum*
glucose-6-phosphate dehydrogenase. WESR5. salt-stress responding gene.

CAA06200.1 AJ004900 *Glycine max*
pentose phosphate pathway oxidoreductase generating NADPH. glucose-6-phosphate-dehydrogenase.

SEQ ID NO: 812

BAA08910.1 D50407 *Cucumis sativus*
glutamyl-tRNA reductase. hemaA.

AAD16897.1 AF105221 *Glycine max*
converts glutamyl-tRNA to glutamate 1-semialdehyde. glutamyl-tRNA reductase precursor. gtr1.

BAA11091.1 D67088 *Cucumis sativus*
glutamyl-tRNA reductase. hemaA2.

BAA25003.1 AB011416 *Oryza sativa*
glutamyl-tRNA reductase.

AAG13620.1 AC078840 *Oryza sativa*
putative glutamyl-tRNA reductase. OSJNBb0073N24.1.

CAA60054.1 X86101 *Hordeum vulgare*
aminolevulinate synthesis (chlorophyll synthesis). glutamyl tRNA reductase. hemaA 1. 1st isoform.

CAA63140.1 X92403 *Hordeum vulgare*
glutamyl-tRNA reductase. hemaA1. isoform I.

BAA25167.1 D88382 *Hordeum vulgare*
glutamyl-tRNA reductase. hemaA1. isoform 1.

CAA60055.1 X86102 *Hordeum vulgare*
aminolevulinate synthesis (chlorophyll synthesis). glutamyl tRNA reductase. hemaA 2. 2nd isoform.

BAA25168.1 D88383 *Hordeum vulgare*
glutamyl-tRNA reductase. hemaA3. isoform 3.

AAG41962.1 AF305613 *Chlamydomonas reinhardtii*
glutamyl-tRNA reductase precursor. HemaA. pGtr.

AAG02480.1 AF294753 *Hordeum vulgare*
converts glutamyl-tRNA to glutamate 1-semialdehyde in the chlorophyll biosynthetic pathway. glutamyl-tRNA reductase. hemaA2.

AAG02479.1 AF294752 *Hordeum vulgare*
converts glutamyl-tRNA to glutamate 1-semialdehyde in the chlorophyll biosynthetic pathway. glutamyl-tRNA reductase. hemA1.

SEQ ID NO: 813

BAA82556.1 AB030083 *Populus nigra*
lectin-like protein kinase. PnLPK.

AAD21872.1 AF078082 *Phaseolus vulgaris*
receptor-like protein kinase homolog RK20-1.

AAF43408.1 AF230515 *Oryza sativa* subsp. *japonica*
serine/threonine protein kinase. YK35.

CAB51480.1 Y14600 *Sorghum bicolor*
putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.

CAA73134.1 Y12531 *Brassica oleracea*
serine/threonine kinase. BRLK.

AAB93834.1 U82481 *Zea mays*
KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.

AAK00425.1 AC069324 *Oryza sativa*
Putative protein kinase. OSJNBa0071K19.11.

BAA92954.1 AP001551 *Oryza sativa*
Similar to *Oryza sativa* protein kinase (OSPK10) mRNA. (L27821).

BAB39873.1 AP002882 *Oryza sativa*
putative protein kinase. P0439B06.8. contains ESTs
AU056701(S20808),AU056702(S20808).

BAB19337.1 AP003044 *Oryza sativa*
putative protein kinase. P0038C05.10. contains ESTs
AU056335(S20481),AU056336(S20481).

AAK21965.1 AY028699 *Brassica napus*
receptor protein kinase PERK1.

BAA92953.1 AP001551 *Oryza sativa*
Similar to *Arabidopsis thaliana* chromosome 4 BAC clone F10M6 ; S-receptor kinase -like protein. (AL021811).

BAB07906.1 AP002835 *Oryza sativa*
putative S-receptor kinase. P0417G05.14.

BAA94516.1 AP001800 *Oryza sativa*
Similar to *Zea mays* S-domain receptor-like protein kinase (AJ010166).

AAD52097.1 AF088885 *Nicotiana tabacum*
receptor-like kinase CHRK1. Chrk1.

BAB21240.1 AP002953 *Oryza sativa*
Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).

AAC23542.1 U20948 *Ipomoea trifida*
receptor protein kinase. IRK1.

BAB18292.1	AP002860	Oryza sativa	putative receptor-like protein kinase. P0409B08.19.
AAG16628.1	AY007545	Brassica napus	protein serine/threonine kinase BNK1.
AAA33915.1	L27821	Oryza sativa	receptor type serine/threonine kinase. protein kinase.
BAB03429.1	AP002817	Oryza sativa	EST C22619(S11214) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).
BAB07999.1	AP002525	Oryza sativa	putative protein kinase. P0462H08.22. contains EST C22619(S11214).
BAA94509.1	AB041503	Populus nigra	protein kinase 1. PnPK1.
AAD46420.1	AF100771	Hordeum vulgare	receptor-like kinase. Hv3ARK. similar to wheat ARK1AS.
BAA23676.1	AB000970	Brassica rapa	receptor kinase 1. BcRK1.
AAD38286.1	AC007789	Oryza sativa	putative protein kinase. OSJNBa0049B20.13.
BAB40081.1	AP003074	Oryza sativa	putative receptor protein kinase. OSJNBa0004G10.30.
BAB18321.1	AP002865	Oryza sativa	putative receptor protein kinase. P0034C11.11.
BAA94517.1	AP001800	Oryza sativa	Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAA21132.1	D88193	Brassica rapa	S-receptor kinase. SRK9 (B.c).
BAA06285.1	D30049	Brassica rapa	S-receptor kinase SRK9.
BAB07905.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.13.
BAA94529.2	AP001800	Oryza sativa	Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
AAB61708.1	U93048	Daucus carota	somatic embryogenesis receptor-like kinase. SERK.
CAA79355.1	Z18921	Brassica oleracea	S-receptor kinase-like protein.
AAK11674.1	AF339747	Lophopyrum elongatum	protein kinase. ESI47.
AAF43496.1	AF131222	Lophopyrum elongatum	protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.

BAA94528.1	AP001800	Oryza sativa	Similar to Arabidopsis thaliana chromosome 2 BAC T20K24; putative receptor-like protein kinase (AC002392).
BAA94510.1	AB041504	Populus nigra	protein kinase 2. PnPK2.
AAA33000.1	M76647	Brassica oleracea	receptor protein kinase. SKR6.
CAA67145.1	X98520	Brassica oleracea	receptor-like kinase. SFR2.
AAB47421.1	U59316	Lycopersicon esculentum	serine/threonine protein kinase Pto. pto. allele of Pto bacterial speck disease resistance gene in tomato.
BAA07577.2	D38564	Brassica rapa	receptor protein kinase SRK12.
AAA33008.1	M97667	Brassica napus	serine/threonine kinase receptor.
CAB89179.1	AJ245479	Brassica napus subsp. napus	ser /thr kinase. S-locus receptor kinase. srk.
BAA92837.1	AB032474	Brassica oleracea	S60 S-locus receptor kinase. SRK60.
SEQ ID NO: 814			
AAF23903.1	AF194416	Oryza sativa	MAP kinase homolog. MAPK2. RMAPK2.
AAD52659.1	AF177392	Oryza sativa	blast and wounding induced mitogen-activated protein kinase. BWMK1. BWMK1 MAP kinase.
AAF23902.1	AF194415	Oryza sativa	MAP kinase homolog. MAPK1. RMAPK1.
AAD28617.1	AF129087	Medicago sativa	mitogen-activated protein kinase homologue. TDY1.
CAB61750.1	AJ275316	Cicer arietinum	MAP kinase protein.
AAB57843.1	U96716	Selaginella lepidophylla	MAP kinase-like protein. sdhn-6r.
AAF65766.1	AF242308	Euphorbia esula	mitogen-activated protein kinase. regulated by tyrosine and threonine phosphorylation.
BAB18271.1	AB035141	Chlamydomonas reinhardtii	mitogen-activated protein kinase. CrMPK2.
CAA58761.1	X83880	Nicotiana tabacum	p45Ntf4 serine/threonine protein kinase. ntf4.
CAA47099.1	X66469	Medicago sativa	MAP Kinase. MSK7.

AAB41548.1	L07042	Medicago sativa	autophosphorylating serine/threonine protein kinase. MAP kinase. MsERK1.
AAB58396.1	U94192	Nicotiana tabacum	salicylic acid-activated MAP kinase. NtSIPK.
CAA50036.1	X70703	Pisum sativum	MAP kinase homologue. PSMAPKIN.
AAF73236.1	AF153061	Pisum sativum	MAP kinase 3. Mapk3. PsMAPK3.
BAB32406.1	AB055515	Nicotiana tabacum	NRK1 MAPK. nrk1. A tobacco MAPK that is phosphorylated and activated by NQK1.
CAA58760.1	X83879	Nicotiana tabacum	p43Ntf6 serine/threonine protein kinase. ntf6.
CAA57721.1	X82270	Medicago sativa	protein kinase. MMK4.
AAF81420.1	AF247136	Capsicum annuum	MAP kinase 2. MK2. CAMK2; wound, UV-C, and cold-inducible expression.
AAD37790.1	AF149424	Ipomoea batatas	MAP kinase.
AAG40580.1	AF216316	Oryza sativa	MAP kinase 2. protein kinase; MAP2.
CAB37188.1	AJ224336	Medicago sativa	MAP kinase. MMK3.
AAF61238.1	AF241166	Oryza sativa	MAP kinase MAPK2.
AAG40581.1	AF216317	Oryza sativa	MAP kinase 3. protein kinase; MAP3.
CAB61889.1	AJ251330	Oryza sativa	protein kinase. MAPK4 protein. mapk4.
CAA73323.1	Y12785	Petroselinum crispum	MAP kinase I.
CAC13967.1	AJ250311	Oryza sativa	protein kinase. MAPK2 protein. mapk2.
CAA56314.1	X79993	Avena sativa	MAP KINASE. Asmap1.
CAA49592.1	X69971	Nicotiana tabacum	serine/threonine protein kinase. NTF3.
CAA58466.1	X83440	Petunia x hybrida	MAP/ERK kinase 1. MEK1.
AAK01710.1	AF332873	Oryza sativa	MAP kinase BIMK1.
AAG40579.1	AF216315	Oryza sativa	MAP kinase 1. protein kinase; MAP1.

CAA57719.1	X82268	Medicago sativa	protein kinase. MMK2.
AAC28850.1	AF079318	Triticum aestivum	protein kinase. MAP kinase homolog. WCK-1.
AAD32204.1	AF134730	Prunus armeniaca	putative mitogen-activated protein kinase MAPK. MAP kinase.
BAA74734.1	AB016802	Zea mays	MAP kinase 5. ZmMPK5.
AAF73257.1	AF154329	Pisum sativum	MAP kinase PsMAPK2. Mapk2.
BAA09600.1	D61377	Nicotiana tabacum	WIPK. MAP (mitogen-activated protein) kinase.
AAF81419.1	AF247135	Capsicum annuum	MAP kinase 1. MK1. wound and UV-C inducible expression.
BAA74733.1	AB016801	Zea mays	MAP kinase 4. ZmMPK4.
CAA05328.1	AJ002314	Nicotiana tabacum	serine/threonine protein kinase. shaggy-like kinase 111. NSK 111.
CAA05329.1	AJ002315	Nicotiana tabacum	shaggy-like kinase 59. NSK 59.
CAA11861.1	AJ224164	Petunia x hybrida	shaggy kinase 6. PSK6.
CAA58595.1	X83620	Petunia x hybrida	Petunia Shaggy kinase 6. PSK6.
CAA11862.1	AJ224165	Petunia x hybrida	shaggy kinase 7. PSK7.
CAA58594.1	X83619	Petunia x hybrida	Petunia Shaggy kinase 4. PSK4.
AAA92823.1	U18365	Brassica napus	cyclin dependent protein kinase homolog; similar to moth bean p34cdc2 protein, PIR Accession Number JQ2243.
BAA92214.1	AP001278	Oryza sativa	ESTs C22403(C50132),C22404(C50132) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana shaggy related protein kinase ASK-gamma. (P43289).
CAA67554.1	X99100	Trifolium repens	protein kinase. trK.
SEQ ID NO: 816			
CAA65065.1	X95759	Solanum tuberosum	glycogen (starch) synthase.
CAA64173.1	X94400	Solanum tuberosum	soluble-starch-synthase. SSSIII.

AAC14014.1	AF023159	Zea mays	starch synthase DULL1. dull1. similar to potato starch synthase SSIII; likely to be the maize starch synthase defined biochemically as SSII.
CAB40374.1	AJ225088	Vigna unguiculata	ADP-glucose-starch glucosyltransferase. Starch synthase isoform SS III.
AAF88000.1	AF258609	Aegilops tauschii	starch synthase III.
AAF87999.1	AF258608	Triticum aestivum	starch synthase III. wSSIII.
CAB40375.1	AJ006752	Vigna unguiculata	ADP-glucose starch glucosyltransferase. starch synthase, isoform V.
AAC14015.1	AF023160	Zea mays	starch synthase DULL1. dull1. similar to potato starch synthase SSIII; like to be the maize starch synthase defined biochemically as SSII.
AAC17971.2	AF026422	Chlamydomonas reinhardtii	soluble starch synthase. ADP-glucose:alpha-1, 4-D-glucan-4-alpha-D-glucosyltransferase.
AAD13342.1	AF019297	Zea mays	starch synthase isoform zSTSII-2. zSSIIb.
CAB86618.1	AJ269502	Triticum aestivum	transfers the glucosyl unit of ADP glucose to the non-reducing end of an alpha 1,4. starch synthase IIa-1. wSs2a-1.
CAA61269.1	X88790	Pisum sativum	glycogen (starch) synthase.
CAB96626.1	AJ269503	Triticum aestivum	transfers the glucosyl unit of ADP glucose to the non-reducing end of an alpha 1,4. starch synthase IIa-2. wSs2a-2.
CAB96627.1	AJ269504	Triticum aestivum	transfers the glucosyl unit of ADP glucose to the non-reducing end of an alpha 1,4. starch synthase IIa-3. wSs2a-3.
CAA71442.1	Y10416	Solanum tuberosum	soluble starch (bacterial glycogen) synthase. SS I.
AAD53263.1	AF155217	Triticum aestivum	starch synthase IIA.
AAF37876.1	AF234163	Hordeum vulgare	starch synthase I. SSI.
CAB99209.1	AJ292521	Triticum aestivum	essential for starch synthesis. starch synthase I-1. wSsI-1.
AAD54661.1	AF091803	Triticum aestivum	starch synthase I.
AAB17085.1	U66377	Triticum aestivum	starch synthase. TaSS. EC 2.4.1.11.
CAB99210.1	AJ292522	Triticum aestivum	essential for starch synthesis. starch synthase I-2. wSsI-2.

AAF03557.1	AF091802	<i>Aegilops tauschii</i> starch synthase I.
AAD13341.1	AF019296	<i>Zea mays</i> starch synthase isoform zSTSII-1. zSSIIa.
AAC17969.2	AF026420	<i>Chlamydomonas reinhardtii</i> ADP-Glucose:alpha-1, 4-D-glucan-4-alpha-D-glucosyltransferase. granule-bound starch synthase I precursor. STA2. GBSSI.
BAA82346.1	AB029546	<i>Phaseolus vulgaris</i> granule-bound starch synthase I. GBSSI.
CAA37732.1	X53694	<i>Oryza sativa</i> starch synthase.
CAA52273.1	X74160	<i>Manihot esculenta</i> starch (bacterial glycogen) synthase. GBSS.
AAF72561.1	AF141954	<i>Oryza sativa</i> granule-bound starch synthase. Waxy.
CAA46294.1	X65183	<i>Oryza sativa</i> glycogen (starch) synthase. waxy gene. starch granule enzyme.
AAF72562.1	AF141955	<i>Oryza sativa</i> granule-bound starch synthase. Waxy.
CAA44065.1	X62134	<i>Oryza sativa</i> starch biosynthesis. starch (bacterial glycogen) synthase. Wx.
AAB02197.1	U48227	<i>Triticum aestivum</i> soluble starch synthase.
AAF13168.1	AF173900	<i>Manihot esculenta</i> granule bound starch synthase II precursor. GBSSII. MEGBSSII.
CAA45472.1	X64108	<i>Oryza sativa</i> starch granule-bound starch synthase. waxy.
AAC61675.2	AF031162	<i>Oryza sativa</i> granule-bound starch synthase. Waxy.
AAC70779.1	AF097922	<i>Astragalus membranaceus</i> granule-bound glycogen (starch) synthase. GBSS.
CAA06958.1	AJ006293	<i>Antirrhinum majus</i> granule-bound starch synthase. waxy.
AAC19119.1	AF068834	<i>Ipomoea batatas</i> starch synthase.
AAD49850.1	AF165890	<i>Oryza sativa</i> subsp. japonica soluble starch synthase.
BAA81848.1	AB026295	<i>Oryza sativa</i> ESTs AU075322(C11109),D22430(C11109) correspond to a region of the predicted gene.; Rice gene for soluble starch synthase (SSS1), complete cds (exon1-15).(D38221).
BAA03739.1	D16202	<i>Oryza sativa</i> soluble starch synthase precursor.

CAA61268.1 X88789 Pisum sativum
glycogen (starch) synthase.

AAA86423.1 U44126 Ipomoea batatas
starch synthase. SPSS67.

AAF14233.1 AF109395 Triticum aestivum
granule-bound starch synthase GBSSII.

CAA41359.1 X58453 Solanum tuberosum
glycogen (starch) synthase. amf. waxy protein, granule-bound starch synthase.

AAG43519.1 AF210699 Perilla frutescens
granule-bound starch synthase. GBSSI. waxy protein.

SEQ ID NO: 819

BAA13032.1 D86180 Pisum sativum
phosphoribosylanthranilate transferase. PAT1.

SEQ ID NO: 822

AAB86850.1 AF031540 Fritillaria agrestis
cytochrome C. cytC.

AAC84135.1 AF101422 Cichorium intybus
cytochrome.

BAA02159.1 D12634 Oryza sativa
'cytochrome C'.

AAA63515.1 M63704 Oryza sativa
cytochrome c. Cc-1.

AAA92712.1 L77113 Helianthus annuus
cytochrome c. cytcl. putative.

AAB70265.1 AF017367 Oryza sativa
cytochrome C.

AAA33084.1 M35173 Chlamydomonas reinhardtii
apocytochrome c (cyc).

CAB16954.1 Z99829 Chlamydomonas reinhardtii
cytochrome c. CYC1.

CAA79708.1 Z21499 Stellaria longipes
mitochondrial cytochrome c.

SEQ ID NO: 823

BAA02159.1 D12634 Oryza sativa
'cytochrome C'.

AAA63515.1 M63704 Oryza sativa
cytochrome c. Cc-1.

AAB86850.1 AF031540 Fritillaria agrestis
cytochrome C. cytC.

AAC84135.1 AF101422 Cichorium intybus
cytochrome.

AAA92712.1	L77113	Helianthus annuus	cytochrome c. cytcl. putative.
AAB70265.1	AF017367	Oryza sativa	cytochrome C.
AAA33084.1	M35173	Chlamydomonas reinhardtii	apocytochrome c (cyc).
CAB16954.1	Z99829	Chlamydomonas reinhardtii	cytochrome c. CYC1.
CAA79708.1	Z21499	Stellaria longipes	mitochondrial cytochrome c.
SEQ ID NO: 825			
BAB17113.1	AP002866	Oryza sativa	putative white protein; ATP-binding cassette transporter. P0410E01.34.
AAF43869.1	AF166114	Chloroplast Mesostigma viride	probable transport protein. cysA.
BAA90508.1	AP001111	Oryza sativa	similar to ABC transporter of Arabidopsis thaliana (AC004697).
AAD54843.1	AF137379	Chloroplast Nephroselmis olivacea	probable transport protein. cysA.
BAA57907.1	AB001684	Chlorella vulgaris	sulfate transport system permease protein. cysA.
BAA90507.1	AP001111	Oryza sativa	similar to ABC transporter of Arabidopsis thaliana (AC004697).
BAB40032.1	AP003046	Oryza sativa	putative ABC transporter. P0445D12.3.
AAG49003.1	AY013246	Hordeum vulgare	putative ABC transporter. 635P2.4b; GC splice donor confirmed by cDNA alignment and comparative sequence.
BAB21275.1	AP002844	Oryza sativa	putative ABC transporter protein. P0410E03.6.
AAG45492.1	AY013245	Oryza sativa	36I5.4. putative ABC transporter; GC splice donor confirmed by cDNA alignment and comparative sequence.
AAG49002.1	AY013246	Hordeum vulgare	putative ABC transporter. 635P2.4a; GC splice donor confirmed by cDNA and comparative sequencing.
BAB21276.1	AP002844	Oryza sativa	putative ABC transporter protein. P0410E03.7. contains EST D22472(C1173).
AAD10836.1	U52079	Solanum tuberosum	P-glycoprotein. pmdrl. binds ATP; ATPase; transporter; transmembrane protein.
BAB21279.1	AP002844	Oryza sativa	putative ABC transporter protein. P0410E03.10. contains ESTs AU065360(R3463),AU101680(R3463).

BAB21273.1 AP002844 *Oryza sativa*
putative ABC transporter protein. P0410E03.4.

BAA83352.1 AP000391 *Oryza sativa*
ESTs AU067992(C11433),AU077424(C11433) correspond to a region of the predicted gene.;
Similar to ABC transporter-7 (U43892).

BAA96612.1 AP002482 *Oryza sativa*
Similar to *Arabidopsis thaliana* chromosome 2, BAC F14M4 ; putative ABC transporter
(AC004411).

SEQ ID NO: 827

AAG34803.1 AF243368 *Glycine max*
glutathione S-transferase GST 13.

AAG16758.1 AY007560 *Lycopersicon esculentum*
putative glutathione S-transferase T3.

AAG34798.1 AF243363 *Glycine max*
glutathione S-transferase GST 8.

AAF64450.1 AF239928 *Euphorbia esula*
glutathione S-transferase. similar to auxin-inducible GST.

AAG34807.1 AF243372 *Glycine max*
glutathione S-transferase GST 17.

AAG34796.1 AF243361 *Glycine max*
glutathione S-transferase GST 6.

AAG16759.1 AY007561 *Lycopersicon esculentum*
putative glutathione S-transferase T4.

AAG34797.1 AF243362 *Glycine max*
glutathione S-transferase GST 7.

AAG34801.1 AF243366 *Glycine max*
glutathione S-transferase GST 11.

AAG34804.1 AF243369 *Glycine max*
glutathione S-transferase GST 14.

AAG34809.1 AF243374 *Glycine max*
glutathione S-transferase GST 19.

AAG34808.1 AF243373 *Glycine max*
glutathione S-transferase GST 18.

AAG34810.1 AF243375 *Glycine max*
glutathione S-transferase GST 20.

AAG16757.1 AY007559 *Lycopersicon esculentum*
putative glutathione S-transferase T2.

AAG16756.1 AY007558 *Lycopersicon esculentum*
putative glutathione S-transferase T1.

AAG34844.1 AF244701 *Zea mays*
glutathione S-transferase GST 36.

AAG34805.1 AF243370 *Glycine max*
glutathione S-transferase GST 15.

AAG34831.1	AF244688	Zea mays	glutathione S-transferase GST 23.
AAG34832.1	AF244689	Zea mays	glutathione S-transferase GST 24.
AAG34849.1	AF244706	Zea mays	glutathione S-transferase GST 41.
AAG34802.1	AF243367	Glycine max	glutathione S-transferase GST 12.
CAA09187.1	AJ010448	Alopecurus myosuroides	glutathione transferase. GST1a.
AAG34829.1	AF244686	Zea mays	glutathione S-transferase GST 21.
CAA09188.1	AJ010449	Alopecurus myosuroides	glutathione transferase. GST1b.
AAA68430.1	J03679	Solanum tuberosum	glutathione S-transferase. gst1. previously called pathogenesis-related protein; prp1-1.
AAG34836.1	AF244693	Zea mays	glutathione S-transferase GST 28.
AAG34837.1	AF244694	Zea mays	glutathione S-transferase GST 29.
AAG34800.1	AF243365	Glycine max	glutathione S-transferase GST 10.
AAC18566.1	AF048978	Glycine max	2,4-D inducible glutathione S-transferase. GSTa.
AAC32118.1	AF051214	Picea mariana	probable glutathione S-transferase. Sb18. similar to Nicotiana tabacum probable glutathione S-transferase encoded by GenBank Accession Number X56266.
AAF22517.1	AF118924	Papaver somniferum	glutathione S-transferase 1. GST1.
AAF22518.1	AF118925	Papaver somniferum	glutathione S-transferase 2. GST2.
AAG32471.1	AF309378	Oryza sativa subsp. japonica	putative glutathione S-transferase OsGSTU4.
AAG34806.1	AF243371	Glycine max	glutathione S-transferase GST 16.
CAA04391.1	AJ000923	Carica papaya	glutathione transferase. PGST1.
AAG32472.1	AF309379	Oryza sativa subsp. japonica	putative glutathione S-transferase OsGSTU3.
AAG34833.1	AF244690	Zea mays	glutathione S-transferase GST 25.
CAA71784.1	Y10820	Glycine max	glutathione transferase.

AAG34847.1 AF244704 Zea mays
glutathione S-transferase GST 39.

AAF22519.1 AF118926 Papaver somniferum
glutathione S-transferase 3. GST3.

SEQ ID NO: 828

AAG34803.1 AF243368 Glycine max
glutathione S-transferase GST 13.

AAG34797.1 AF243362 Glycine max
glutathione S-transferase GST 7.

AAG34798.1 AF243363 Glycine max
glutathione S-transferase GST 8.

AAF64450.1 AF239928 Euphorbia esula
glutathione S-transferase. similar to auxin-inducible GST.

AAG16758.1 AY007560 Lycopersicon esculentum
putative glutathione S-transferase T3.

AAG34796.1 AF243361 Glycine max
glutathione S-transferase GST 6.

AAG16759.1 AY007561 Lycopersicon esculentum
putative glutathione S-transferase T4.

AAG34801.1 AF243366 Glycine max
glutathione S-transferase GST 11.

AAG34804.1 AF243369 Glycine max
glutathione S-transferase GST 14.

AAG34807.1 AF243372 Glycine max
glutathione S-transferase GST 17.

AAG34809.1 AF243374 Glycine max
glutathione S-transferase GST 19.

AAG34810.1 AF243375 Glycine max
glutathione S-transferase GST 20.

AAG16757.1 AY007559 Lycopersicon esculentum
putative glutathione S-transferase T2.

AAG16756.1 AY007558 Lycopersicon esculentum
putative glutathione S-transferase T1.

AAG34802.1 AF243367 Glycine max
glutathione S-transferase GST 12.

AAG34808.1 AF243373 Glycine max
glutathione S-transferase GST 18.

AAG34844.1 AF244701 Zea mays
glutathione S-transferase GST 36.

CAA09188.1 AJ010449 Alopecurus myosuroides
glutathione transferase. GST1b.

CAA09187.1	AJ010448	<i>Alopecurus myosuroides</i> glutathione transferase. GST1a.
AAG32472.1	AF309379	<i>Oryza sativa</i> subsp. <i>japonica</i> putative glutathione S-transferase OsGSTU3.
AAA68430.1	J03679	<i>Solanum tuberosum</i> glutathione S-transferase. <i>gst1</i> . previously called pathogenesis-related protein; <i>prp1-1</i> .
AAG34837.1	AF244694	<i>Zea mays</i> glutathione S-transferase GST 29.
AAG34800.1	AF243365	<i>Glycine max</i> glutathione S-transferase GST 10.
AAG34831.1	AF244688	<i>Zea mays</i> glutathione S-transferase GST 23.
AAC32118.1	AF051214	<i>Picea mariana</i> probable glutathione S-transferase. Sb18. similar to <i>Nicotiana tabacum</i> probable glutathione S-transferase encoded by GenBank Accession Number X56266.
AAG34805.1	AF243370	<i>Glycine max</i> glutathione S-transferase GST 15.
AAC18566.1	AF048978	<i>Glycine max</i> 2,4-D inducible glutathione S-transferase. GSTa.
AAG34829.1	AF244686	<i>Zea mays</i> glutathione S-transferase GST 21.
CAA04391.1	AJ000923	<i>Carica papaya</i> glutathione transferase. PGST1.
CAA71784.1	Y10820	<i>Glycine max</i> glutathione transferase.
AAG34795.1	AF243360	<i>Glycine max</i> glutathione S-transferase GST 5.
AAG34836.1	AF244693	<i>Zea mays</i> glutathione S-transferase GST 28.
AAG34832.1	AF244689	<i>Zea mays</i> glutathione S-transferase GST 24.
AAG34833.1	AF244690	<i>Zea mays</i> glutathione S-transferase GST 25.
AAG34849.1	AF244706	<i>Zea mays</i> glutathione S-transferase GST 41.
AAG34806.1	AF243371	<i>Glycine max</i> glutathione S-transferase GST 16.
CAA09189.1	AJ010450	<i>Alopecurus myosuroides</i> glutathione transferase. GST1c.
SEQ ID NO: 829		
AAG34803.1	AF243368	<i>Glycine max</i> glutathione S-transferase GST 13.

AAF64450.1	AF239928	<i>Euphorbia esula</i> glutathione S-transferase. similar to auxin-inducible GST.
AAG16758.1	AY007560	<i>Lycopersicon esculentum</i> putative glutathione S-transferase T3.
AAG34798.1	AF243363	<i>Glycine max</i> glutathione S-transferase GST 8.
AAG34801.1	AF243366	<i>Glycine max</i> glutathione S-transferase GST 11.
AAG34797.1	AF243362	<i>Glycine max</i> glutathione S-transferase GST 7.
AAG34796.1	AF243361	<i>Glycine max</i> glutathione S-transferase GST 6.
AAG34807.1	AF243372	<i>Glycine max</i> glutathione S-transferase GST 17.
AAG16759.1	AY007561	<i>Lycopersicon esculentum</i> putative glutathione S-transferase T4.
AAG34804.1	AF243369	<i>Glycine max</i> glutathione S-transferase GST 14.
AAG34810.1	AF243375	<i>Glycine max</i> glutathione S-transferase GST 20.
AAG34809.1	AF243374	<i>Glycine max</i> glutathione S-transferase GST 19.
AAG16757.1	AY007559	<i>Lycopersicon esculentum</i> putative glutathione S-transferase T2.
AAG16756.1	AY007558	<i>Lycopersicon esculentum</i> putative glutathione S-transferase T1.
AAG34805.1	AF243370	<i>Glycine max</i> glutathione S-transferase GST 15.
AAC18566.1	AF048978	<i>Glycine max</i> 2,4-D inducible glutathione S-transferase. GSTa.
AAG34808.1	AF243373	<i>Glycine max</i> glutathione S-transferase GST 18.
AAG34800.1	AF243365	<i>Glycine max</i> glutathione S-transferase GST 10.
AAG34829.1	AF244686	<i>Zea mays</i> glutathione S-transferase GST 21.
AAG34802.1	AF243367	<i>Glycine max</i> glutathione S-transferase GST 12.
AAG34837.1	AF244694	<i>Zea mays</i> glutathione S-transferase GST 29.
CAA09187.1	AJ010448	<i>Alopecurus myosuroides</i> glutathione transferase. GST1a.

CAA09188.1	AJ010449	<i>Alopecurus myosuroides</i>	glutathione transferase. GST1b.
AAG34849.1	AF244706	<i>Zea mays</i>	glutathione S-transferase GST 41.
AAG34844.1	AF244701	<i>Zea mays</i>	glutathione S-transferase GST 36.
AAG34806.1	AF243371	<i>Glycine max</i>	glutathione S-transferase GST 16.
CAA71784.1	Y10820	<i>Glycine max</i>	glutathione transferase.
AAA68430.1	J03679	<i>Solanum tuberosum</i>	glutathione S-transferase. gst1. previously called pathogenesis-related protein; prp1-1.
CAA04391.1	AJ000923	<i>Carica papaya</i>	glutathione transferase. PGST1.
AAG34836.1	AF244693	<i>Zea mays</i>	glutathione S-transferase GST 28.
AAG34831.1	AF244688	<i>Zea mays</i>	glutathione S-transferase GST 23.
AAG34847.1	AF244704	<i>Zea mays</i>	glutathione S-transferase GST 39.
AAC32118.1	AF051214	<i>Picea mariana</i>	probable glutathione S-transferase. Sb18. similar to <i>Nicotiana tabacum</i> probable glutathione S-transferase encoded by GenBank Accession Number X56266.
AAF29773.1	AF159229	<i>Gossypium hirsutum</i>	glutathione S-transferase. GST.
AAG32472.1	AF309379	<i>Oryza sativa</i> subsp. <i>japonica</i>	putative glutathione S-transferase OsGSTU3.
AAG41204.1	AF321437	<i>Suaeda maritima</i>	glutathione transferase.
CAC24549.1	AJ296343	<i>Cichorium intybus</i> x <i>Cichorium endivia</i>	glutathione S-transferase. chi-GST1. auxin-induced GST.

SEQ ID NO: 830

AAD37699.1	AF145730	<i>Oryza sativa</i>	homeodomain leucine zipper protein. Oshox6. transcription factor.
BAA93461.1	AB028073	<i>Physcomitrella patens</i>	homeobox protein PpHB2. PpHB2. homeodomain-leucine zipper gene.
AAF01765.1	AF184278	<i>Glycine max</i>	homeodomain-leucine zipper protein 57. Hdl57. transcription factor.
AAF01764.2	AF184277	<i>Glycine max</i>	homeodomain-leucine zipper protein 56. Hdl56. transcription factor.
BAA93466.1	AB028078	<i>Physcomitrella patens</i>	homeobox protein PpHB7. PpHB7. homeodomain-leucine zipper gene.

CAB67118.1	Y17306	<i>Lycopersicon esculentum</i>	homeodomain protein. h52.
AAF73482.1	AF268422	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	hb-6-like protein. transcription factor; similar to <i>Arabidopsis thaliana</i> hb-6 protein.
AAD37697.1	AF145728	<i>Oryza sativa</i>	homeodomain leucine zipper protein. Oshox4. transcription factor.
BAA21017.1	D26578	<i>Daucus carota</i>	transcriptional regulator. DNA-binding protein. homeodomain at nt 761-940; leucine zipper at nt 941-1048.
BAA05624.1	D26575	<i>Daucus carota</i>	transcriptional regulator. DNA-binding protein. homeodomain at nt 520-699; leucine zipper at nt 700-805.
BAA93460.1	AB028072	<i>Physcomitrella patens</i>	homeobox protein PpHB1. PpHB1. homeodomain-leucine zipper gene.
BAA93464.1	AB028076	<i>Physcomitrella patens</i>	homeobox protein PpHB5. PpHB5. homeodomain-leucine zipper gene.
BAA93467.1	AB028079	<i>Physcomitrella patens</i>	homeobox protein PpHB8. PpHB8. homeodomain-leucine zipper gene.
BAA93465.1	AB028077	<i>Physcomitrella patens</i>	homeobox protein PpHB6. PpHB6. homeodomain-leucine zipper gene.
BAA05625.1	D26576	<i>Daucus carota</i>	transcriptional regulator. DNA-binding protein. homeodomain at nt 300-479; leucine zipper at nt 480-587.
BAA93468.1	AB028080	<i>Physcomitrella patens</i>	homeobox protein PpHB9. PpHB9. homeodomain-leucine zipper gene.
BAA05623.1	D26574	<i>Daucus carota</i>	transcriptional regulator. DNA-binding protein. homeodomain at nt 498-677; leucine zipper at nt 678-785.
BAA05622.1	D26573	<i>Daucus carota</i>	transcriptional regulator. DNA-binding protein. homeodomain at nt 585-764; leucine zipper at nt 765-851.
AAD37698.1	AF145729	<i>Oryza sativa</i>	homeodomain leucine zipper protein. Oshox5. transcription factor.
CAA64221.1	X94449	<i>Pimpinella brachycarpa</i>	transcription activator. homeobox-leucine zipper protein. PHZ4.
CAA64152.1	X94375	<i>Pimpinella brachycarpa</i>	transcription activator. homeobox-leucine zipper protein.
CAA64491.1	X95193	<i>Pimpinella brachycarpa</i>	transcription activator. homeobox-leucine zipper protein.
BAA93463.1	AB028075	<i>Physcomitrella patens</i>	homeobox protein PpHB4. PpHB4. homeodomain-leucine zipper gene.
CAA06728.1	AJ005833	<i>Craterostigma plantagineum</i>	transcription factor. homeodomain leucine zipper protein. hb-2.

AAD37695.1 AF145726 *Oryza sativa*
homeodomain leucine zipper protein. Oshox2. transcription factor.

CAA65456.2 X96681 *Oryza sativa*
transcription factor. DNA-binding protein. Oshox1. homeodomain leucine zipper gene.

AAF19980.1 AF211193 *Oryza sativa*
homeodomain-leucine zipper transcription factor. Hox1. hox1.

AAK31270.1 AC079890 *Oryza sativa*
homeodomain leucine zipper protein hox1. OSJNBb0089A17.12.

CAA63222.1 X92489 *Glycine max*
transcription activator. homeobox-leucine zipper protein.

CAA06717.1 AJ005820 *Craterostigma plantagineum*
transcription factor. homeodomain leucine zipper protein. hb-1.

AAA79778.1 L48485 *Helianthus annuus*
homeodomain protein. putative.

SEQ ID NO: 831

CAA06334.1 AJ005077 *Lycopersicon esculentum*
protein kinase. TCTR2 protein. TCTR2.

AAG31141.1 AF305911 *Oryza sativa*
EDR1. EDR1. MAP kinase kinase kinase; similar to *Arabidopsis thaliana* EDR1.

AAG31142.1 AF305912 *Hordeum vulgare*
EDR1. EDR1. MAP kinase kinase kinase; similar to *Arabidopsis thaliana* EDR1.

AAK30005.1 AY029067 *Rosa* hybrid cultivar
CTR2 protein kinase.

AAD46406.1 AF096250 *Lycopersicon esculentum*
ethylene-responsive protein kinase TCTR1. ER50. serine/threonine kinase; similar to *Arabidopsis thaliana* negative regulator of the ethylene response pathway encoded by GenBank Accession Number L08789.

CAA73722.1 Y13273 *Lycopersicon esculentum*
putative protein kinase.

AAD10057.1 AF110519 *Lycopersicon esculentum*
ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit ripening inducible CTR1-like protein kinase; TCTR1v.

AAD10056.1 AF110518 *Lycopersicon esculentum*
ethylene-inducible CTR1-like protein kinase. protein kinase homolog; ethylene and fruit ripening inducible CTR1-like protein kinase; TCTR1.

AAA34002.1 M67449 *Glycine max*
protein kinase. PK6.

AAK11734.1 AY027437 *Arachis hypogaea*
serine/threonine/tyrosine kinase.

BAB16918.1 AP002863 *Oryza sativa*
putative protein kinase. P0005A05.22.

CAC09580.1 AJ298992 *Fagus sylvatica*
Absciscic acid (ABA) and calcium induced protein kinase. protein kinase (PK). pk1.

CAA97692.1	Z73295	Catharanthus roseus	receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
AAF59906.1	AF197947	Glycine max	receptor protein kinase-like protein. CLV1B.
AAF59905.1	AF197946	Glycine max	receptor protein kinase-like protein. CLV1A.
AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.
BAA87852.1	AP000816	Oryza sativa	Similar to putative Ser/Thr protein kinase. (AC004218).
BAB40094.1	AP003210	Oryza sativa	putative receptor protein kinase. OSJNBa0010K01.7.
BAA92221.1	AP001278	Oryza sativa	Similar to Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).
CAA08995.1	AJ010091	Brassica napus	MAP3K alpha 1 protein kinase. MAP3K alpha 1.
BAB21240.1	AP002953	Oryza sativa	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
CAB51834.1	00069	Oryza sativa	11332.5. contains eukaryotic protein kinase domain PF.
CAA08997.1	AJ010093	Brassica napus	MAP3K beta 1 protein kinase. MAP3K beta 1.
CAB54520.1	AJ238845	Brassica napus	putative role in cell cycle control. MAP3K epsilon 1 protein kinase. MAP3Kel.
AAF34436.1	AF172282	Oryza sativa	similar to mitogen-activated protein kinases. DUPR11.32.
BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
AAG25966.1	AF302082	Nicotiana tabacum	cytokinin-regulated kinase 1. CRK1. protein kinase; transcript abundance decreases rapidly after cytokinin treatment.
BAA06538.1	D31737	Nicotiana tabacum	protein-serine/threonine kinase.
AAF76189.1	AF271206	Rosa hybrid cultivar	CTR1-like protein kinase. Raf-like protein kinase.
BAA84787.1	AP000559	Oryza sativa	ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).

BAA83373.1 AP000391 *Oryza sativa*
ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).

AAF66615.1 AF142596 *Nicotiana tabacum*
LRR receptor-like protein kinase.

AAF91322.1 AF244888 *Glycine max*
receptor-like protein kinase 1. RLK1. GmRLK1.

AAD21872.1 AF078082 *Phaseolus vulgaris*
receptor-like protein kinase homolog RK20-1.

CAA61510.1 X89226 *Oryza sativa*
leucine-rich repeat/receptor protein kinase. lrk2.

BAA87853.1 AP000816 *Oryza sativa*
EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).

AAF91323.1 AF244889 *Glycine max*
receptor-like protein kinase 2. RLK2. GmRLK2.

AAF91324.1 AF244890 *Glycine max*
receptor-like protein kinase 3. RLK3. GmRLK3.

AAF43394.1 AF230501 *Oryza sativa* subsp. *japonica*
serine/threonine protein kinase. YK1.

AAK16409.1 AF320086 *Zea mays*
serine threonine kinase 1. stk1. expressed in mature tassel.

AAK21965.1 AY028699 *Brassica napus*
receptor protein kinase PERK1.

BAB39437.1 AP003338 *Oryza sativa*
receptor-like kinase. OJ1212_B09.6.

AAK11568.1 AF318492 *Lycopersicon hirsutum*
Pto-like protein kinase B. LhirPtoB.

SEQ ID NO: 832

AAF35901.1 AF230332 *Zinnia elegans*
expansin 2.

CAC19184.1 AJ291817 *Cicer arietinum*
expansin.

AAG13982.1 AF297521 *Prunus avium*
expansin 1. Exp1. PruavExp1.

BAB19676.1 AB029083 *Prunus persica*
expansin. PchExp1.

AAC33529.1 U93167 *Prunus armeniaca*
expansin. PA-Exp1.

AAC33530.1 AF038815 *Prunus armeniaca*
expansin. Exp2.

AAD47901.1 AF085330 *Pinus taeda*
expansin.

AAB37746.1	U30382	Cucumis sativus	expansin S1 precursor. Cs-EXP1. similar to pollen allergen Lol pI, Lolium perenne, Swiss-Prot Accession Number P14946; former gene name CuExS1; expansin-29 (Ex29) protein.
AAF21101.1	AF159563	Fragaria x ananassa	expansin. Exp2. ripening regulated.
AAB40634.1	U64890	Pinus taeda	expansin. similar to Arabidopsis expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to Cucumis sativus expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.
AAB40637.1	U64893	Pinus taeda	expansin. similar to Arabidopsis expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to Cucumis sativus expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.
AAB40635.1	U64891	Pinus taeda	expansin. similar to Arabidopsis expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to Cucumis sativus expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.
CAB43197.1	AJ239068	Lycopersicon esculentum	cell wall loosening enzyme. expansin2. exp2.
AAB40636.1	U64892	Pinus taeda	expansin. similar to Arabidopsis expansin encoded by GenBank Accession Numbers U30476, U30478, U30480 and U30481, to Cucumis sativus expansin encoded by GenBank Accession Numbers U30382 and U30460, and to rice expansin encoded by GenBank Accession Numbers U30477 and U30479.
AAC64201.1	AF096776	Lycopersicon esculentum	expansin. LeEXP2.
AAD49956.1	AF167360	Rumex palustris	expansin. EXP1.
AAC96081.1	AF049354	Nicotiana tabacum	involved in acid-growth response. alpha-expansin precursor. Nt-EXP5. cell wall protein.
AAC39512.1	AF043284	Gossypium hirsutum	expansin. GhEX1. contains N-terminal signal peptide.
AAB81662.1	U85246	Oryza sativa	expansin. Os-EXP4.
AAG13983.1	AF297522	Prunus avium	expansin 2. Exp2. PruavExp2.
AAF32409.1	AF230276	Triphysaria versicolor	alpha-expansin 3.
AAG32921.1	AF184233	Lycopersicon esculentum	expansin. Exp10.

BAB32732.1	AB049406	<i>Eustoma grandiflorum</i> expansin. Eg Expansin.
AAF32411.1	AF230278	<i>Triphysaria versicolor</i> alpha-expansin 1.
AAF35902.1	AF230333	<i>Zinnia elegans</i> expansin 3.
AAB38074.1	U30477	<i>Oryza sativa</i> induces extension (creep) in plant cell walls. expansin Os-EXP2. Os-EXP2. former gene name RiExB.
AAC96080.1	AF049353	<i>Nicotiana tabacum</i> involved in acid-growth response. alpha-expansin precursor. Nt-EXP4. cell wall protein.
AAF17570.1	AF202119	<i>Marsilea quadrifolia</i> alpha-expansin. EXP1. Mq-EXP1.
CAC06433.1	AJ276007	<i>Festuca pratensis</i> expansin. exp2.
AAD13633.1	AF059489	<i>Lycopersicon esculentum</i> expansin precursor. Exp5.
CAC19183.1	AJ291816	<i>Cicer arietinum</i> expansin.
AAF62181.1	AF247163	<i>Oryza sativa</i> alpha-expansin OsEXP6. cell wall loosening factor; expressed in internodes and leaves.
AAF62180.1	AF247162	<i>Oryza sativa</i> alpha-expansin OsEXP5. cell wall loosening factor; expressed in internodes, leaves, coleoptiles, and roots.
CAB46492.1	AJ243340	<i>Lycopersicon esculentum</i> expansin9. exp9.
BAA88200.1	AP000837	<i>Oryza sativa</i> EST AU078708(E60526) corresponds to a region of the predicted gene. Similar to expansin (U85246).
AAF32410.1	AF230277	<i>Triphysaria versicolor</i> alpha-expansin 2.
AAB37749.1	U30460	<i>Cucumis sativus</i> expansin S2 precursor. Cs-EXP2. similar to pollen allergen Lol pI, <i>Lolium perenne</i> , Swiss-Prot Accession Number P14946; former gene name CuExS2; expansin-30 (Ex30) protein.
CAA04385.1	AJ000885	<i>Brassica napus</i> Cell wall extension in plants. Expansin.
AAF17571.1	AF202120	<i>Regnellidium diphyllum</i> alpha-expansin. EXP1. Rd-EXP1.
AAD13632.1	AF059488	<i>Lycopersicon esculentum</i> expansin precursor. Exp4.
CAA06271.2	AJ004997	<i>Lycopersicon esculentum</i> expansin18. exp18.

AAC63088.1 U82123 *Lycopersicon esculentum*
expansin. LeEXP1. fruit ripening regulated expansin.

AAC96077.1 AF049350 *Nicotiana tabacum*
involved in acid-growth response. alpha-expansin precursor. Nt-EXP1. cell wall protein.

AAF62182.1 AF247164 *Oryza sativa*
alpha-expansin OsEXP7. cell wall loosening factor; expressed in internodes and leaves.

CAC18802.1 AJ289154 *Glycine max*
expansion of cell walls. expansin. dd2/63.

AAC96078.1 AF049351 *Nicotiana tabacum*
involved in acid-growth response. alpha-expansin precursor. Nt-EXP2. cell wall protein.

AAG01875.1 AF291659 *Striga asiatica*
alpha-expansin 3. Exp3.

CAA69105.1 Y07782 *Oryza sativa*
expansin. RiExA.

AAC96079.1 AF049352 *Nicotiana tabacum*
involved in acid-growth response. alpha-expansin precursor. Nt-EXP3. cell wall protein.

SEQ ID NO: 833

AAA34030.1 J03492 *Spinacia oleracea*
glycolate oxidase (EC 1.1.3.15).

AAB40396.1 U80071 *Mesembryanthemum crystallinum*
glycolate oxidase. GOX.

BAA03131.1 D14044 *Cucurbita* sp.
glycolate oxidase.

AAB82143.1 AF022740 *Oryza sativa*
glycolate oxidase. GOX.

CAA63482.1 X92888 *Lycopersicon esculentum*
conversion of glycolate to glyoxylate + H₂O₂. glycolate oxidase.

AAC32392.1 AF082874 *Medicago sativa*
glycolate oxidase.

AAC33509.1 U62485 *Nicotiana tabacum*
photorespiration. glycolate oxidase. GLO.

AAF03097.1 AF162196 *Lactuca sativa*
glycolate oxidase.

SEQ ID NO: 838

CAA06770.1 AJ005928 *Brassica napus*
squalene epoxidase homologue. Sqp1;2.

CAA06773.1 AJ005931 *Brassica napus*
squalene epoxidase homologue. Sqp1;1.

BAA24448.1 AB003516 *Panax ginseng*
squalene epoxidase.

CAA06223.1 AJ004923 *Lycopersicon esculentum*
Squalene epoxidase. ERG.

SEQ ID NO: 840

BAB12686.1 AP002746 *Oryza sativa*
putative pyrophosphate-dependent phosphofructo-1-kinase. P0671B11.1. contains ESTs
AU068014(C11507),C28532(C61484),AU090544(C61415).

BAA99438.1 AP002743 *Oryza sativa*
putative pyrophosphate-dependent phosphofructo-1-kinase. P0710E05.25. contains ESTs
AU068014(C11507),C28532(C61484),AU090544(C61415).

AAB88875.1 U93272 *Prunus armeniaca*
pyrophosphate-dependent phosphofructo-1-kinase.

CAA83683.1 Z32850 *Ricinus communis*
pyrophosphate-dependent phosphofructokinase beta subunit.

AAC67587.1 AF095521 *Citrus x paradisi*
pyrophosphate-dependent phosphofructokinase alpha subunit. PPi-PFKa.

AAA63452.1 M55191 *Solanum tuberosum*
pyrophosphate-fructose 6-phosphate 1-phosphotransferase beta-subunit.

AAC67586.1 AF095520 *Citrus x paradisi*
pyrophosphate-dependent phosphofructokinase beta subunit. PPi-PFKb. PFP.

AAA63451.1 M55190 *Solanum tuberosum*
pyrophosphate-fructose 6-phosphate 1-phosphotransferase alpha-subunit.

CAA83682.1 Z32849 *Ricinus communis*
pyrophosphate-dependent phosphofructokinase alpha subunit.

SEQ ID NO: 841

AAG60182.1 AC084763 *Oryza sativa*
putative ethylene-responsive element binding protein. OSJNBa0027P10.12.

AAK31279.1 AC079890 *Oryza sativa*
putative ethylene-responsive element binding protein. OSJNBb0089A17.16.

AAG43545.1 AF211527 *Nicotiana tabacum*
Avr9/Cf-9 rapidly elicited protein 1. ACRE1. similar to EREBP transcription factors.

AAF63205.1 AF245119 *Mesembryanthemum crystallinum*
AP2-related transcription factor. CDBP. stress induced transcription factor.

BAA07321.1 D38123 *Nicotiana tabacum*
ERF1. ethylene-responsive transcription factor.

BAA97122.1 AB016264 *Nicotiana sylvestris*
ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf2.

CAB93940.1 AJ238740 *Catharanthus roseus*
putative transcription factor. AP2-domain DNA-binding protein. orca2.

BAA87068.1 AB035270 *Matricaria chamomilla*
ethylene-responsive element binding protein1 homolog. McEREBP1.

BAA97124.1 AB016266 *Nicotiana sylvestris*
ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf4.

CAB96900.1	AJ251250	Catharanthus roseus	transcription factor. AP2-domain DNA-binding protein. orca3.
CAB96899.1	AJ251249	Catharanthus roseus	transcription factor. AP2-domain DNA-binding protein. orca3.
AAC62619.1	AF057373	Nicotiana tabacum	transcription factor. ethylene response element binding protein 1. EREBP1.
BAA97123.1	AB016265	Nicotiana glauca	ERF (EREBP); ethylene-responsive element binding factor for basic PR (Pathogenesis-related) gene of higher plant. ethylene-responsive element binding factor. nserf3.
AAC24587.1	AF071893	Prunus armeniaca	AP2 domain containing protein. AP2DCP.
CAC12822.1	AJ299252	Nicotiana tabacum	AP2 domain-containing transcription factor. ap2.
AAF76898.1	AF274033	Atriplex hortensis	apetala2 domain-containing protein.
BAA94514.2	AP001800	Oryza sativa	Similar to Arabidopsis thaliana chromosome 4, BAC clone F9D16; putative Ap2 domain protein (AL035394).
AAC14323.1	AF058827	Nicotiana tabacum	TSI1. Tsi1. contains putative AP2 DNA-binding domain; similar to Pti6.
AAD00708.1	U91857	Stylosanthes hamata	ethylene-responsive element binding protein homolog. similar to EREBP1, -2, -3 and -4 proteins encoded by GenBank Accession Numbers D38123, D38126, D38124, and D38125 respectively.
BAA76734.1	AB024575	Nicotiana tabacum	ethylene responsive element binding factor.
BAB03248.1	AB037183	Oryza sativa	ERF protein transcriptional repressor. ethylene responsive element binding factor3. osERF3.
BAB16083.1	AB036883	Oryza sativa	transcriptional repressor. osERF3. osERF3. ERF protein family ERF3 associated repression domain.
AAF23899.1	AF193803	Oryza sativa	transcription factor EREBP1. EREBP/AP2-like transcription factor.
AAF05606.1	AF190770	Oryza sativa	EREBP-like protein. tsh1. TSH1; induced by ethylene.
CAB93939.1	AJ238739	Catharanthus roseus	putative transcription factor. AP2-domain DNA-binding protein. orca1.
BAA78738.1	AB023482	Oryza sativa	EST AU055776(S20048) corresponds to a region of the predicted gene.; Similar to Arabidopsis thaliana AP2 domain containing protein RAP2.10 mRNA, partial cds.(AF003103).
AAG43548.1	AF211530	Nicotiana tabacum	Avr9/Cf-9 rapidly elicited protein 111A. ACRE111A. similar to EREBP transcription factors.

AAG43549.1	AF211531	Nicotiana tabacum	Avr9/Cf-9 rapidly elicited protein 111B. ACRE111B. similar to EREBP transcription factors.
BAA99376.1	AP002526	Oryza sativa	ESTs AU093391(E60370),AU091593(C60458), AU093392(E60370) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana BAC F21J9; AP2 domain protein. (AC000103).
AAK31271.1	AC079890	Oryza sativa	putative transcriptional factor. OSJNBb0089A17.22.
AAK01089.1	AF298231	Hordeum vulgare	CBF3-like protein BCBF3. BCBF3. AP2 domain protein; DRE binding factor.
AAG59618.1	AF239616	Hordeum vulgare	CRT/DRE-binding factor. CBF.
AAC49567.1	U41466	Zea mays	Glossy15. Glossy15. AP2 DNA-binding domain protein; similar to the Arabidopsis floral homeotic gene APETALA2; maize AP2-domain regulator of leaf epidermal traits; homeotic regulator of leaf epidermal cell identity; allele: W64A; putative transcription factor.
SEQ ID NO: 842			
AAC32034.1	AF023472	Hordeum vulgare	peptide transporter. ptr1. PTR1; integral membrane protein.
BAB40113.1	AP003311	Oryza sativa	putative peptide transport protein. P0024G09.4. contains ESTs D40448(S2437),C71800(E0368),AU102190(E2393), AU055921(S20154),AU102191(E2393),AU055922(S20154), C98524(E0368),AU097146(S2437).
BAB16458.1	AP002483	Oryza sativa	putative peptide transport protein. P0019D06.16. contains ESTs D40448(S2437),C71800(E0368),AU102190(E2393), AU055921(S20154),AU102191(E2393),AU055922(S20154), C98524(E0368),AU097146(S2437).
AAD01600.1	AF016713	Lycopersicon esculentum	LeOPT1. LeOPT1. oligopeptide transporter.
AAF07875.1	AF140606	Oryza sativa	nitrate transporter. NRT1.
AAF20002.1	AF213936	Prunus dulcis	amino acid/peptide transporter. PTR2. similar to transporters of nitrogenous compounds.
AAG46153.1	AC018727	Oryza sativa	putative peptide transporter. OSJNBa0056G17.8.
CAC00544.1	AJ277084	Nicotiana plumbaginifolia	ion transport. putative low-affinity nitrate transporter. nrt1.1.
CAC00545.1	AJ277085	Nicotiana plumbaginifolia	ion transport. putative low-affinity nitrate transporter. nrt1.2.
AAA80582.1	U17987	Brassica napus	putative nitrate transporter. RCH2 protein.

CAC07206.1	AJ278966	Brassica napus	Low-affinity nitrate transporter. nitrate transporter. nrt1.
AAG21898.1	AC026815	Oryza sativa	putative peptide transport protein. OSJNBa0079L16.13.
BAB19758.1	AB052786	Glycine max	putative nitrate transporter NRT1-3. NRT1-3.
AAK15441.1	AC037426	Oryza sativa	putative nitrate transporter. OSJNBb0014I11.9.
AAG21906.1	AC026815	Oryza sativa	putative peptide transport protein. OSJNBa0079L16.9.
BAB19760.1	AB052788	Glycine max	nitrate transporter NRT1-5. NRT1-5.
AAG46154.1	AC018727	Oryza sativa	putative peptide transporter. OSJNBa0056G17.27.
BAB19757.1	AB052785	Glycine max	nitrate transporter NRT1-2. NRT1-2.
BAB19756.1	AB052784	Glycine max	nitrate transporter NRT1-1. NRT1-1.
BAB16322.1	AP002818	Oryza sativa	putative peptide transporter-like protein. P0436E04.4.
AAB69642.1	AF000392	Lotus japonicus	peptide transporter. LjNOD65.
CAA93316.1	Z69370	Cucumis sativus	nitrite transporter. NiTR1.
AAD16016.1	AF080545	Nepenthes alata	peptide transporter. PTR1.
BAB19759.1	AB052787	Glycine max	putative nitrate transporter NRT1-4. NRT1-4.
AAD42860.1	AF154930	Prunus dulcis	transporter-like protein. TLP1.

SEQ ID NO: 847

CAA61980.1	X89890	Bidens pilosa	Calmodulin.
AAF73157.1	AF150059	Brassica napus	calmodulin. CaM1. involved in seed germination.
BAA87825.1	AP000815	Oryza sativa	ESTs AU030013(E50493),AU081341(E50493) correspond to a region of the predicted gene. Similar to O.sativa gene encoding calmodulin. (Z12828).
CAA67054.1	X98404	Capsicum annuum	calmodulin-2.
AAA87347.1	M88307	Brassica juncea	calmodulin.

AAA33397.1	L18912	Lilium longiflorum	calcium binding protein, signal transduction. calmodulin. putative.
AAG27432.1	AF295637	Elaeis guineensis	calmodulin.
CAA42423.1	X59751	Daucus carota	calmodulin. Ccam-1.
AAG11418.1	AF292108	Prunus avium	calmodulin.
AAA92681.1	U13882	Pisum sativum	calcium-binding protein. calmodulin.
AAB46588.1	U83402	Capsicum annuum	calmodulin.
AAA33706.1	M80836	Petunia x hybrida	calmodulin. CAM81.
AAF65511.1	AF108889	Capsicum annuum	calmodulin.
CAA43143.1	X60738	Malus x domestica	Calmodulin. CaM.
AAA19571.1	U10150	Brassica napus	calcium binding. calmodulin. bcml.
CAA78301.1	Z12839	Lilium longiflorum	calcium binding protein, signal transduction. calmodulin.
BAA88540.1	AP000969	Oryza sativa	ESTs AU081349(E61253), D41425(S3918) correspond to a region of the predicted gene. Similar to calmodulin. (AF042840).
AAB36130.1	S81594	Vigna radiata	auxin-regulated calmodulin. auxin-regulated calmodulin, arCaM. This sequence comes from Fig. 1; arCaM.
AAC36059.1	AF042840	Oryza sativa	calmodulin. CaM1.
AAA33901.1	L18913	Oryza sativa	calcium binding protein, signal transduction. calmodulin. putative.
AAA33900.1	L18914	Oryza sativa	calcium binding protein, signal transduction. calmodulin.
AAA34237.1	L20691	Vigna radiata	calmodulin.
CAA78288.1	Z12828	Oryza sativa	calcium binding protein, signal transduction. calmodulin.
AAA32938.1	M27303	Hordeum vulgare	calmodulin.
CAA78287.1	Z12827	Oryza sativa	calcium binding protein, signal transduction. calmodulin.

AAC49587.1	U49105	Triticum aestivum calmodulin TaCaM4-1. calcium-binding protein.
AAC49586.1	U49104	Triticum aestivum calmodulin TaCaM3-3. calcium-binding protein.
AAC49583.1	U48692	Triticum aestivum calmodulin TaCaM2-3. calcium-binding protein.
AAC49585.1	U49103	Triticum aestivum calmodulin TaCaM3-2. calcium-binding protein.
AAC49584.1	U48693	Triticum aestivum calmodulin TaCaM3-1. calcium-binding protein.
AAC49582.1	U48691	Triticum aestivum calmodulin TaCaM2-2. calcium-binding protein.
AAC49580.1	U48689	Triticum aestivum calmodulin TaCaM1-3. calcium-binding protein.
AAC49579.1	U48688	Triticum aestivum calmodulin TaCaM1-2. calcium binding protein.
AAC49578.1	U48242	Triticum aestivum calmodulin TaCaM1-1. calcium-binding.
AAA03580.1	L01431	Glycine max calcium-binding regulatory protein. calmodulin. SCaM-2. putative.
AAC36058.1	AF042839	Oryza sativa calmodulin. CaM2.
AAA85156.1	U20296	Solanum tuberosum calcium-binding protein. calmodulin.
AAA34014.1	L01432	Glycine max calcium-binding regulatory protein. calmodulin. SCaM-3. putative.
AAD10244.1	AF030032	Phaseolus vulgaris calmodulin. CaM. EF-hand protein; calcium-dependent protein; functions in calcium signal transduction pathways.
CAA36644.1	X52398	Medicago sativa calmodulin (AA 1-149).
AAA85155.1	U20294	Solanum tuberosum calcium-binding protein. calmodulin.
AAB68399.1	U79736	Helianthus annuus calmodulin. HaCaM.
AAA62351.1	U20295	Solanum tuberosum calcium-binding protein. calmodulin.
AAA34238.1	L20507	Vigna radiata calmodulin.
AAA85157.1	U20297	Solanum tuberosum calcium-binding protein. calmodulin.
AAA34013.1	L01430	Glycine max calcium-binding regulatory protein. calmodulin. SCaM-1. putative.

AAA33705.1	M80831	Petunia x hybrida	calmodulin-related protein. CAM53.
CAA74307.1	Y13974	Zea mays	calmodulin.
CAA54583.1	X77397	Zea mays	calmodulin. CaM2.
SEQ ID NO: 848			
CAA06486.1	AJ005340	Linum usitatissimum	IAA amidohydrolase. homolog.
SEQ ID NO: 850			
BAB17350.1	AP002747	Oryza sativa	putative nodulin. P0698G03.34. contains ESTs D39891(S1543),D41717(S4395),AU033037(S1543).
BAA85440.1	AP000616	Oryza sativa	ESTs AU055729(S20023),AU055730(S20023) correspond to a region of the predicted gene.; similar to Medicago nodulin N21-like protein (AC004218).
CAB53493.1	AJ245900	Oryza sativa	CAA303720.1 protein. q3037.20. Similar to Medicago nodulin N21 (MtN21).
SEQ ID NO: 852			
AAD16018.1	AF081514	Taxus canadensis	prenyltransferase. geranylgeranyl diphosphate synthase. geranylgeranyl pyrophosphate synthase.
SEQ ID NO: 853			
BAB32588.1	AB055807	Momordica charantia	inhibitor against trypsin. bgit.
AAA34180.1	J05094	Lycopersicon peruvianum	proteinase inhibitor I precursor.
AAA34198.1	M59427	Lycopersicon peruvianum	proteinase inhibitor I. proteinase inhibitor I.
CAB61327.1	AJ132473	Amaranthus hypochondriacus	Proteinase inhibition. trypsin inhibitor.
AAA60745.1	J04099	Lycopersicon esculentum	proteinase inhibitor I. ER1.
CAA78269.1	Z12623	Nicotiana tabacum	Putative precursor of serine proteinase inhibitor type I. Pre-pro-proteinase inhibitor I.
CAA47461.1	X67076	Nicotiana tabacum	inhibitor of microbial serine proteinases (major isoform). TIMPa.
CAA78265.1	Z12619	Nicotiana tabacum	precursor for serine proteinase inhibitor I. Pre-pro-proteinase inhibitor I.
CAA47460.1	X67075	Nicotiana tabacum	inhibitor of microbial serine proteinases (minor isoform). TIMPb.
AAA34067.1	M74102	Nicotiana sylvestris	pre-pro-proteinase inhibitor I.

AAC49603.1	U30861	Solanum tuberosum	serine proteinase inhibitor. wound-inducible proteinase inhibitor I.
BAA02823.1	D13662	Nicotiana glauca X Nicotiana langsdorffii	genetic tumor-related proteinase inhibitor I precursor. GTI.
AAA34199.1	K03290	Lycopersicon esculentum	wound-induced proteinase inhibitor I prepropeptide.
AAA34200.1	M13938	Lycopersicon esculentum	proteinase inhibitor I. PIIF.
AAA69780.1	L06137	Solanum tuberosum	proteinase inhibitor I. pin1. putative.
AAA72133.1	L06985	Solanum tuberosum	proteinase inhibitor I. pin1. The 'a' of the first atg is missing.
CAA78259.1	Z12611	Solanum tuberosum	proteinase inhibitor I.
AAA69781.1	L06606	Solanum tuberosum	proteinase inhibitor I. precursor.
CAA48136.1	X67950	Solanum tuberosum	protease inhibitor I. pin1.
CAA47907.1	X67675	Solanum tuberosum	proteinase inhibitor I. pin1.
CAB71340.1	AJ250663	Hordeum vulgare	putative proteinase inhibitor. bci-7. similarity to subtilisin/chymotrypsin inhibitor.
CAA57677.1	X82187	Zea mays	serine proteinase inhibitor. substilin /chymotrypsin-like inhibitor. pis7.
CAA55588.1	X78988	Zea mays	proteinase inhibitor. MPI.
CAA49593.1	X69972	Zea mays	proteinase inhibitor. MPI.
AAA33816.1	M17108	Solanum tuberosum	proteinase inhibitor I. precursor.
CAA57307.1	X81647	Cucurbita maxima	Pumpkin fruit trypsin inhibitor. pfiAF4.
CAA57203.1	X81447	Cucurbita maxima	Pumpkin Fruit Chymotrypsin Inhibitor. pfiBM7.
SEQ ID NO: 859			
AAC34855.1	AF082030	Hemerocallis hybrid cultivar	senescence-associated protein 5. SA5. mRNA accumulates in senescing petals and accumulation is induced by exogenous ABA.
AAG13616.1	AC078840	Oryza sativa	putative senescence-associated protein. OSJNBb0073N24.21.
SEQ ID NO: 864			
AAF62403.1	AF212183	Nicotiana tabacum	harpin inducing protein. hin1. similar to hin1 protein.

CAA68848.1 Y07563 *Nicotiana tabacum*
activated during hypersensitive response. hin1.

AAB97367.1 AF039532 *Oryza sativa*
harpin induced gene 1 homolog. Hin1.

SEQ ID NO: 871

AAC61839.1 AF025430 *Papaver somniferum*
berberine bridge enzyme. bbe1. (S)-reticuline:oxygen oxidoreductase (methylene bridge forming).

AAB20352.1 S65550 *Eschscholzia californica*
(S)-reticuline:oxygen oxidoreductase (methylene-bridge-forming). /gene="(S)-reticuline:oxygen oxidoreductase. This sequence comes from Fig 2; berberine bridge enzyme.

AAC39358.1 AF005655 *Eschscholzia californica*
oxidizes the N-methyl group of (S)-reticuline to the berberine bridge carbon C-8 of (S)-scoulerine in berberine and benzophenanthridine alkaloid biosynthesis. berberine bridge enzyme. bbe1. covalently-bound FAD-dependent oxidase; elicitor-inducible.

AAD17487.1 AF049347 *Berberis stolonifera*
Catalyzes the oxidative cyclization of the N-methyl group of (S)-reticuline into the berberine bridge carbon (C-8) of (S)-scoulerine. berberine bridge enzyme. bbe1. Covalently flavinylated oxidase of isoquinoline alkaloid biosynthesis in plants.

SEQ ID NO: 872

AAF98369.1 AF158253 *Nicotiana tabacum*
patatin-like protein 3. PAT3. NtPat3.

CAA73328.1 Y12793 *Cucumis sativus*
mobilization of fat during seed germination. patatin-like protein.

CAA11042.1 AJ223039 *Hevea brasiliensis*
latex allergen. sequence similarity to patatins.

AAF25553.1 AF113546 *Hevea brasiliensis*
latex protein allergen Hev b 7. putative PLA2; similar to *Solanum tubulin* patatin encoded by GenBank Accession Number X03932.

CAA11041.1 AJ223038 *Hevea brasiliensis*
latex allergen. with sequence similarity to patatins.

AAC27724.1 U80598 *Hevea brasiliensis*
latex patatin homolog. putative PLA2; latex protein allergen; similar to *Solanum tubulin* patatin encoded by GenBank Accession Number X03932.

AAK27797.1 AF318315 *Vigna unguiculata*
patatin-like protein.

AAK18751.1 AF193067 *Vigna unguiculata*
patatin-like protein.

AAB08428.1 U68484 *Nicotiana tabacum*
patatin homolog.

AAD22170.1 AF061282 *Sorghum bicolor*
patatin-like protein.

AAF98368.1 AF158027 *Nicotiana tabacum*
 patatin-like protein 1. PAT1. NtPat1.

AAD22169.1 AF061282 *Sorghum bicolor*
 patatin-like protein.

CAA81735.1 Z27221 *Solanum tuberosum*
 patatin.

CAA31575.1 X13178 *Solanum tuberosum*
 patatin B2 (AA 1 - 386).

AAA33819.1 M18880 *Solanum tuberosum*
 patatin.

CAA31576.1 X13179 *Solanum tuberosum*
 patatin B1 (377 AA) (1 is 3rd base in codon).

CAA27588.1 X03956 *Solanum tuberosum*
 patatin.

AAA33828.1 M21879 *Solanum tuberosum*
 patatin.

CAA27571.1 X03932 *Solanum tuberosum*
 patatin.

CAA25592.1 X01125 *Solanum tuberosum*
 patatin.

AAA66198.1 U09331 *Solanum brevidens*
 patatin precursor.

AAB08427.1 U68483 *Nicotiana tabacum*
 patatin homolog.

AAF98370.1 AF158254 *Nicotiana tabacum*
 patatin-like protein 2. PAT2.

AAD22149.1 AF061282 *Sorghum bicolor*
 patatin-like protein. similar to the EST sequences E0496(panicle at flowering stage), R2382
 (root), R2382 (root), S4036 (shoot), S3728 (shoot), S13457 (green shoot).

SEQ ID NO: 875

BAA93022.1 AP001552 *Oryza sativa*
 ESTs C74776(E51022), C26123(C116681) correspond to a region of the predicted gene.
 Similar to *Arabidopsis thaliana* cultivar Landsberg extra-large G-protein (AF060942).

SEQ ID NO: 876

BAA87853.1 AP000816 *Oryza sativa*
 EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative
 NAK-like Ser/Thr protein kinase. (AF001308).

AAK21965.1 AY028699 *Brassica napus*
 receptor protein kinase PERK1.

AAD21872.1 AF078082 *Phaseolus vulgaris*
 receptor-like protein kinase homolog RK20-1.

AAK00425.1 AC069324 *Oryza sativa*
 Putative protein kinase. OSJNBa0071K19.11.

BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808), AU056702(S20808).
AAA33915.1	L27821	Oryza sativa	receptor type serine/threonine kinase. protein kinase.
BAA82556.1	AB030083	Populus nigra	lectin-like protein kinase. PnLPK.
AAK11674.1	AF339747	Lophopyrum elongatum	protein kinase. ESI47.
AAF43496.1	AF131222	Lophopyrum elongatum	protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.
AAG59657.1	AC084319	Oryza sativa	putative protein kinase. OSJNBa0004B24.20.
AAG03090.1	AC073405	Oryza sativa	Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).
AAB93834.1	U82481	Zea mays	KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
AAF66615.1	AF142596	Nicotiana tabacum	LRR receptor-like protein kinase.
AAG25966.1	AF302082	Nicotiana tabacum	cytokinin-regulated kinase 1. CRK1. protein kinase; transcript abundance decreases rapidly after cytokinin treatment.
AAB09771.1	U67422	Zea mays	CRINKLY4 precursor. cr4. receptor kinase homolog.
AAF34428.1	AF172282	Oryza sativa	receptor-like protein kinase. DUPR11.18.
BAB07906.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.14.
AAC23542.1	U20948	Ipomoea trifida	receptor protein kinase. IRK1.
BAA94516.1	AP001800	Oryza sativa	Similar to Zea mays S-domain receptor-like protein kinase (AJ010166).
BAA87852.1	AP000816	Oryza sativa	Similar to putative Ser/Thr protein kinase. (AC004218).
BAA92221.1	AP001278	Oryza sativa	Similar to Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).
CAA73134.1	Y12531	Brassica oleracea	serine/threonine kinase. BRLK.
BAA92954.1	AP001551	Oryza sativa	Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).

AAG16628.1	AY007545	Brassica napus	protein serine/threonine kinase BNK1.
CAB51834.1	00069	Oryza sativa	11332.5. contains eukaryotic protein kinase domain PF.
BAA06538.1	D31737	Nicotiana tabacum	protein-serine/threonine kinase.
CAA73133.1	Y12530	Brassica oleracea	serine /threonine kinase. ARLK.
CAB89179.1	AJ245479	Brassica napus subsp. napus	ser /thr kinase. S-locus receptor kinase. srk.
AAA33008.1	M97667	Brassica napus	serine/threonine kinase receptor.
BAA92837.1	AB032474	Brassica oleracea	S60 S-locus receptor kinase. SRK60.
AAA33000.1	M76647	Brassica oleracea	receptor protein kinase. SKR6.
CAA79355.1	Z18921	Brassica oleracea	S-receptor kinase-like protein.
CAA67145.1	X98520	Brassica oleracea	receptor-like kinase. SFR2.
CAA74661.1	Y14285	Brassica oleracea	SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.
AAA62232.1	U00443	Brassica napus	S-receptor kinase. protein contains an immunoglobulin-like domain.
BAA23676.1	AB000970	Brassica rapa	receptor kinase 1. BcRK1.
BAB07904.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.12.
BAA94518.1	AP001800	Oryza sativa	Similar to Arabidopsis thaliana chromosome 2 section 111 of 255; putative receptor-like protein kinase (AC002392).
BAA07577.2	D38564	Brassica rapa	receptor protein kinase SRK12.
CAA74662.1	Y14286	Brassica oleracea	SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
BAA07576.1	D38563	Brassica rapa	receptor protein kinase SRK8.
BAB07999.1	AP002525	Oryza sativa	putative protein kinase. P0462H08.22. contains EST C22619(S11214).
BAB07905.1	AP002835	Oryza sativa	putative S-receptor kinase. P0417G05.13.

BAB03429.1 AP002817 *Oryza sativa*
EST C22619(S11214) corresponds to a region of the predicted gene. Similar to *Arabidopsis thaliana* chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).

SEQ ID NO: 883

BAA90510.2 AP001111 *Oryza sativa*
rice EST AU030811, similar to rice Ca²⁺-ATPase (U82966).

AAF73985.1 AF096871 *Zea mays*
calcium pump. calcium ATPase. cap1.

CAA63790.1 X93592 *Dunaliella bioculata*
P-type ATPase. cal. calcium pumping; CA1.

AAD11618.1 AF050496 *Lycopersicon esculentum*
Ca²⁺-ATPase. LCA1B; alternative transcript.

AAA34138.1 M96324 *Lycopersicon esculentum*
The calcium ATPase is a calcium ion pump. Ca²⁺-ATPase. LCA1.

AAB58910.1 U82966 *Oryza sativa*
Ca²⁺-ATPase.

AAD11617.1 AF050495 *Lycopersicon esculentum*
Ca²⁺-ATPase. LCA1A; alternative transcript.

AAG28435.1 AF195028 *Glycine max*
plasma membrane Ca²⁺-ATPase. SCA1.

AAG28436.1 AF195029 *Glycine max*
plasma membrane Ca²⁺-ATPase. SCA2.

CAA68234.1 X99972 *Brassica oleracea*
calmodulin-stimulated calcium-ATPase.

AAD31896.1 AF145478 *Mesembryanthemum crystallinum*
calcium ATPase.

AAB60276.1 U09989 *Zea mays*
H(+)-transporting ATPase. Mha1.

CAB69824.1 AJ271439 *Prunus persica*
plasma membrane H⁺ ATPase. PPA1.

AAD46187.1 AF156683 *Nicotiana glauca*
plasma membrane proton ATPase. pma8.

BAA01058.1 D10207 *Oryza sativa*
H-ATPase. OSA1.

AAB49042.1 U54690 *Dunaliella acidophila*
plasma membrane proton ATPase. dha1. DaDHA1; proton pump.

AAA34173.1 M60166 *Lycopersicon esculentum*
H⁺-ATPase. LHA1.

CAA52107.1 X73901 *Dunaliella bioculata*
plasma membrane ATPase. pma1.

AAB35314.2	S79323	Vicia faba	plasma membrane H(+)-ATPase precursor. plasma membrane H(+)-ATPase. This sequence comes from Fig. 1; conceptual translation presented here differs from translation in publication.
BAA06629.1	D31843	Oryza sativa	plasma membrane H ⁺ -ATPase. OSA2.
AAA34094.1	M80489	Nicotiana plumbaginifolia	plasma membrane H ⁺ ATPase. pma1.
BAA08134.1	D45189	Zostera marina	plasma membrane H ⁺ -ATPase. zha1.
CAB85494.1	AJ132891	Medicago truncatula	proton pump. H ⁺ -ATPase. ha1.
CAB85495.1	AJ132892	Medicago truncatula	proton pump. H ⁺ -ATPase. ha1.
AAB84202.2	AF029256	Kosteletzkya virginica	plasma membrane proton ATPase. ATP1.
CAA47275.1	X66737	Nicotiana plumbaginifolia	plasma membrane H ⁺ -ATPase. pma4.
CAA54045.1	X76535	Solanum tuberosum	H(+)-transporting ATPase. PHA2.
AAD46186.1	AF156679	Nicotiana plumbaginifolia	plasma membrane proton ATPase. pma6.
AAB17186.1	U72148	Lycopersicon esculentum	plasma membrane H ⁺ -ATPase. LHA4. plasma membrane proton pumping ATPase.
CAB69823.1	AJ271438	Prunus persica	plasma membrane H ⁺ ATPase. PPA2.
AAB41898.1	U84891	Mesembryanthemum crystallinum	plasma membrane proton pump. H ⁺ -transporting ATPase. PMA.
CAC29436.1	AJ310524	Vicia faba	P-type H ⁺ -ATPase. ha5. predominantly expressed in guard cells and flowers.
BAA37150.1	AB022442	Vicia faba	p-type H ⁺ -ATPase. VHA2.
CAA59800.1	X85805	Zea mays	H(+)-transporting ATPase. MHA-2.
CAA59799.1	X85804	Phaseolus vulgaris	H(+)-transporting ATPase. BHA-1.
CAC29435.1	AJ310523	Vicia faba	P-type H ⁺ -ATPase. vha4. predominantly expressed in flowers.
AAD46188.1	AF156691	Nicotiana plumbaginifolia	plasma membrane proton ATPase. pma9.
AAA34099.1	M80491	Nicotiana plumbaginifolia	plasma membrane H ⁺ ATPase. pma3.

AAA34052.1	M27888	Nicotiana plumbaginifolia	H ⁺ -translocating ATPase.
CAA54046.1	X76536	Solanum tuberosum	H(+)-transporting ATPase. PHA1.
AAA34098.1	M80490	Nicotiana plumbaginifolia	plasma membrane H ⁺ ATPase. pma3.
AAD55399.1	AF179442	Lycopersicon esculentum	plasma membrane H ⁺ -ATPase isoform LHA2. LHA2.
AAF98344.1	AF275745	Lycopersicon esculentum	plasma membrane H ⁺ -ATPase. LHA2. P-type ion pump.
AAG01028.1	AF289025	Cucumis sativus	plasma membrane H ⁺ -ATPase.
AAK31799.1	AY029190	Lilium longiflorum	plasma membrane H ⁺ ATPase. LILHA1.
AAA81348.1	U38965	Vicia faba	p-type H ⁺ -ATPase. VHA2.
AAK32119.1	AF308817	Hordeum vulgare	plasmalemma H ⁺ -ATPase 2.
AAK32118.1	AF308816	Hordeum vulgare	plasmalemma H ⁺ -ATPase 1.
AAA20600.1	U08984	Zea mays	plasma-membrane H ⁺ ATPase. Zmpma1.
SEQ ID NO: 884			
AAD21872.1	AF078082	Phaseolus vulgaris	receptor-like protein kinase homolog RK20-1.
AAB93834.1	U82481	Zea mays	KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
CAA73134.1	Y12531	Brassica oleracea	serine/threonine kinase. BRLK.
AAC23542.1	U20948	Ipomoea trifida	receptor protein kinase. IRK1.
CAA67145.1	X98520	Brassica oleracea	receptor-like kinase. SFR2.
CAA73133.1	Y12530	Brassica oleracea	serine /threonine kinase. ARLK.
BAA23676.1	AB000970	Brassica rapa	receptor kinase 1. BcRK1.
CAB41879.1	Y18260	Brassica oleracea	SRK15 protein. SRK15. receptor-like kinase.
CAB41878.1	Y18259	Brassica oleracea	SRK5 protein. SRK5. receptor-like kinase.

CAA74662.1	Y14286	Brassica oleracea	SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
CAA74661.1	Y14285	Brassica oleracea	SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.
BAA06285.1	D30049	Brassica rapa	S-receptor kinase SRK9.
BAA21132.1	D88193	Brassica rapa	S-receptor kinase. SRK9 (B.c).
BAA92836.1	AB032473	Brassica oleracea	S18 S-locus receptor kinase. SRK18.
CAA79355.1	Z18921	Brassica oleracea	S-receptor kinase-like protein.
AAA33000.1	M76647	Brassica oleracea	receptor protein kinase. SKR6.
AAA62232.1	U00443	Brassica napus	S-receptor kinase. protein contains an immunoglobulin-like domain.
AAA33008.1	M97667	Brassica napus	serine/threonine kinase receptor.
CAB89179.1	AJ245479	Brassica napus subsp. napus	ser /thr kinase. S-locus receptor kinase. srk.
BAB18292.1	AP002860	Oryza sativa	putative receptor-like protein kinase. P0409B08.19.
AAD52097.1	AF088885	Nicotiana tabacum	receptor-like kinase CHRK1. Chrk1.
BAA92837.1	AB032474	Brassica oleracea	S60 S-locus receptor kinase. SRK60.
BAB21001.1	AB054061	Brassica rapa	S locus receptor kinase. SRK22.
BAA07576.1	D38563	Brassica rapa	receptor protein kinase SRK8.
BAA07577.2	D38564	Brassica rapa	receptor protein kinase SRK12.
AAK02023.1	AC074283	Oryza sativa	Putative protein kinase-like. OSJNBa0087H07.5.
CAA79324.1	Z18884	Brassica oleracea	S-receptor kinase related protein.
BAB16871.1	AP002537	Oryza sativa	putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).

BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
AAK21965.1	AY028699	Brassica napus	receptor protein kinase PERK1.
BAA87853.1	AP000816	Oryza sativa	EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
CAB51836.1	AJ243961	Oryza sativa	Putitive Ser/Thr protein kinase. l1332.7.
AAA33915.1	L27821	Oryza sativa	receptor type serine/threonine kinase. protein kinase.
BAB21240.1	AP002953	Oryza sativa	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.
BAA92954.1	AP001551	Oryza sativa	Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).
AAF66615.1	AF142596	Nicotiana tabacum	LRR receptor-like protein kinase.
BAB17139.1	AP002867	Oryza sativa	putative receptor kinase. P0463F06.31.
SEQ ID NO: 885			
CAA80358.1	Z22645	Solanum tuberosum	cleavage of sucrose to glucose and fructose. beta-fructofuranosidase.
CAA79676.1	Z21486	Solanum tuberosum	cleavage of sucrose to glucose and fructose. beta-fructofuranosidase.
CAA57428.1	X81834	Nicotiana tabacum	beta-fructofuranosidase. Ntbfruc1. beta-fructosidase.
CAA49162.1	X69321	Daucus carota	beta-fructofuranosidase. Inva1*DC1.
CAA57389.1	X81792	Chenopodium rubrum	beta-fructofuranosidase. CIN1.
AAC17166.1	AF063246	Pisum sativum	hydrolyzes sucrose to glucose and fructose. cell wall invertase. bfruct1. isoform Pcl-2; the Pcl-1 isoform is in the file with GenBank Accession Number X85327; beta-fructofuranosidase.
CAA59677.1	X85327	Pisum sativum	hydrplyze sucrose into fructose and glucose. invertase. bfruct1. beta-fructofuranosidase.
AAD02263.1	AF043346	Zea mays	sucrose hydrolysis. cell wall invertase. incw3. Incw3; beta-fructofuranosidase.
CAA84526.1	Z35162	Vicia faba	hydrolyze sucrose. beta-fructofuranosidase; cell wall invertase I; fructosidase. VFCWINV1.

AAC96065.1	AF030420	Triticum aestivum	hydrolyzes sucrose. cell wall invertase. IVR1. hydrolase; beta-fructofuranosidase; fructosidase.
CAA53099.1	X75353	Daucus carota	beta-fructofuranosidase.
AAB68679.1	U92438	Phaseolus vulgaris	soluble acid invertase. PVSAI; potential vacuolar targeted enzyme; beta-fructofuranosidase.
CAA89992.1	Z49831	Vicia faba	hydrolyze sucrose. vacuolar invertase; beta-fructofuranosidase. VFVCINV.
CAA53097.1	X75351	Daucus carota	beta-fructofuranosidase.
CAA77267.1	Y18707	Daucus carota	beta-fructofuranosidase, isoform I. Inv*Dc4. soluble acid invertase.
CAA53098.1	X75352	Daucus carota	beta-fructofuranosidase.
CAA77266.1	Y18706	Daucus carota	beta-fructofuranosidase, isoform II. Inv*Dc5. soluble acid invertase.
AAC96066.1	AF030421	Triticum aestivum	hydrolyzes sucrose. cell wall invertase. IVR3. hydrolase; beta-fructofuranosidase; fructosidase.
AAG36943.1	AF274299	Brassica oleracea	cleaves sucrose into glucose and fructose at acid pH optima. acid invertase AI7-3. sucrose hydrolysing enzyme; beta-fructofuranosidase.
SEQ ID NO: 887			
AAD10836.1	U52079	Solanum tuberosum	P-glycoprotein. pmdr1. binds ATP; ATPase; transporter; transmembrane protein.
BAA96612.1	AP002482	Oryza sativa	Similar to Arabidopsis thaliana chromosome 2, BAC F14M4 ; putative ABC transporter (AC004411).
AAG49002.1	AY013246	Hordeum vulgare	putative ABC transporter. 635P2.4a; GC splice donor confirmed by cDNA and comparative sequencing.
AAG45492.1	AY013245	Oryza sativa	36I5.4. putative ABC transporter; GC splice donor confirmed by cDNA alignment and comparative sequence.
BAA83352.1	AP000391	Oryza sativa	ESTs AU067992(C11433),AU077424(C11433) correspond to a region of the predicted gene.; Similar to ABC transporter-7 (U43892).
AAG49003.1	AY013246	Hordeum vulgare	putative ABC transporter. 635P2.4b; GC splice donor confirmed by cDNA alignment and comparative sequence.
BAB17113.1	AP002866	Oryza sativa	putative white protein; ATP-binding cassette transporter. P0410E01.34.

BAA90508.1	AP001111	Oryza sativa	similar to ABC transporter of Arabidopsis thaliana (AC004697).
BAA90507.1	AP001111	Oryza sativa	similar to ABC transporter of Arabidopsis thaliana (AC004697).
BAB16495.1	AP002861	Oryza sativa	putative ABC transporter ATP-binding protein. P0665D10.21.
BAB21276.1	AP002844	Oryza sativa	putative ABC transporter protein. P0410E03.7. contains EST D22472(C1173).
BAB21275.1	AP002844	Oryza sativa	putative ABC transporter protein. P0410E03.6.
BAB21273.1	AP002844	Oryza sativa	putative ABC transporter protein. P0410E03.4.
BAB40032.1	AP003046	Oryza sativa	putative ABC transporter. P0445D12.3.
SEQ ID NO: 888			
AAD21872.1	AF078082	Phaseolus vulgaris	receptor-like protein kinase homolog RK20-1.
CAA73134.1	Y12531	Brassica oleracea	serine/threonine kinase. BRLK.
AAB93834.1	U82481	Zea mays	KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
AAC23542.1	U20948	Ipomoea trifida	receptor protein kinase. IRK1.
AAA33000.1	M76647	Brassica oleracea	receptor protein kinase. SKR6.
CAB89179.1	AJ245479	Brassica napus subsp. napus	ser /thr kinase. S-locus receptor kinase. srk.
AAA33008.1	M97667	Brassica napus	serine/threonine kinase receptor.
CAA74661.1	Y14285	Brassica oleracea	SFR1. extracellular S domain: 8-1342; transmembrane domain: 1343-1411; intracellular kinase domain: 1412-2554.
CAA67145.1	X98520	Brassica oleracea	receptor-like kinase. SFR2.
AAA62232.1	U00443	Brassica napus	S-receptor kinase. protein contains an immunoglobulin-like domain.
CAA73133.1	Y12530	Brassica oleracea	serine /threonine kinase. ARLK.
BAA23676.1	AB000970	Brassica rapa	receptor kinase 1. BcRK1.
BAA92836.1	AB032473	Brassica oleracea	S18 S-locus receptor kinase. SRK18.

CAA74662.1	Y14286	Brassica oleracea	SFR3. extracellular S domain: 123-1346; transmembrane domain: 1347-1412; intracellular kinase domain: from 1413.
CAA79355.1	Z18921	Brassica oleracea	S-receptor kinase-like protein.
CAB41879.1	Y18260	Brassica oleracea	SRK15 protein. SRK15. receptor-like kinase.
BAA06285.1	D30049	Brassica rapa	S-receptor kinase SRK9.
BAA21132.1	D88193	Brassica rapa	S-receptor kinase. SRK9 (B.c).
CAB41878.1	Y18259	Brassica oleracea	SRK5 protein. SRK5. receptor-like kinase.
BAA92837.1	AB032474	Brassica oleracea	S60 S-locus receptor kinase. SRK60.
BAA07577.2	D38564	Brassica rapa	receptor protein kinase SRK12.
BAB21001.1	AB054061	Brassica rapa	S locus receptor kinase. SRK22.
BAA07576.1	D38563	Brassica rapa	receptor protein kinase SRK8.
AAD52097.1	AF088885	Nicotiana tabacum	receptor-like kinase CHRK1. Chrk1.
AAK02023.1	AC074283	Oryza sativa	Putative protein kinase-like. OSJNBa0087H07.5.
BAB18292.1	AP002860	Oryza sativa	putative receptor-like protein kinase. P0409B08.19.
BAA87853.1	AP000816	Oryza sativa	EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
AAK21965.1	AY028699	Brassica napus	receptor protein kinase PERK1.
BAB21240.1	AP002953	Oryza sativa	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
BAB17331.1	AP002747	Oryza sativa	putative receptor kinase. P0698G03.12.
BAB17139.1	AP002867	Oryza sativa	putative receptor kinase. P0463F06.31.
AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.

BAB16871.1 AP002537 *Oryza sativa*
putative protein kinase APK1A *Arabidopsis thaliana*. P0001B06.24. contains ESTs
C22608(R3192), D25110(R3192).

BAA92954.1 AP001551 *Oryza sativa*
Similar to *Oryza sativa* protein kinase (OSPK10) mRNA. (L27821).

CAB51836.1 AJ243961 *Oryza sativa*
Putitive Ser/Thr protein kinase. I1332.7.

AAF78016.1 AF238472 *Oryza sativa*
receptor-like kinase. RLG15. protein kinase.

BAB39451.1 AP003338 *Oryza sativa*
putative receptor kinase. OJ1212_B09.24.

SEQ ID NO: 890

AAB47181.1 S82324 *Zea mays*
/gene="calcium/calmodulin-dependent protein kinase. This sequence comes from Fig. 1.

BAA22410.1 D38452 *Zea mays*
calcium-dependent protein kinase-related kinase.

BAA12692.1 D84508 *Zea mays*
CDPK-related protein kinase. Does not require calcium for its activity.

AAG01179.1 AF289237 *Zea mays*
calcium/calmodulin dependent protein kinase MCK2. MCK2.

CAA58750.1 X83869 *Daucus carota*
CDPK-related protein kinase. CRK (or PK421).

BAA12691.1 D84507 *Zea mays*
CDPK-related protein kinase. Does not require calcium for its activity (by similarity).

AAC24961.1 AF009337 *Tradescantia virginiana*
CDPK-related protein kinase. CRK1.

AAF23901.2 AF194414 *Oryza sativa*
calcium-dependent protein kinase. CDPK5. OsCDPK5.

AAF23900.1 AF194413 *Oryza sativa*
calcium-dependent protein kinase. CDPK1. OsCDPK1.

AAC78558.1 AF030879 *Solanum tuberosum*
protein kinase CPK1.

AAD17800.1 AF090835 *Mesembryanthemum crystallinum*
Ca²⁺-dependent protein kinase: CPK1. serine/threonine protein kinase.

AAB49984.1 U90262 *Cucurbita pepo*
calcium-dependent calmodulin-independent protein kinase CDPK. cpCPK1. serine/threonine
protein kinase that is activated by direct binding of calcium.

CAA07481.1 AJ007366 *Zea mays*
calcium-dependent protein kinase.

BAB21081.1 AP002819 *Oryza sativa*
putative calcium-dependent protein kinase. P0501G01.10.

BAA12715.1 D85039 *Zea mays*
calcium-dependent protein kinase.

AAC25423.1	AF072908	Nicotiana tabacum	calcium-dependent protein kinase. CDPK1.
CAA39936.1	X56599	Daucus carota	calcium-dependent protein kinase. DcPK431.
CAA57157.1	X81394	Oryza sativa	calcium-dependent protein kinase. OSCP2.
AAF21062.1	AF216527	Dunaliella tertiolecta	calcium-dependent protein kinase. CPK1; CDPK.
BAA81751.1	AB017517	Marchantia polymorpha	calcium-dependent protein kinase. CDPK1. CDPK-B; alternative splicing.
BAA81749.1	AB017515	Marchantia polymorpha	calcium-dependent protein kinase. CDPK1. CDPK-B; alternative splicing.
AAB88537.1	AF035944	Fragaria x ananassa	calcium-dependent protein kinase. MAX17.
BAA81750.1	AB017516	Marchantia polymorpha	calcium-dependent protein kinase. CDPK1. CDPK-A; alternative splicing.
BAA81748.1	AB017515	Marchantia polymorpha	calcium-dependent protein kinase. CDPK1. CDPK-A; alternative splicing.
AAA69507.1	U28376	Zea mays	calcium-dependent protein kinase. MZECDPK2.
AAA61682.1	L27484	Zea mays	calcium-dependent protein kinase. CDPK.
AAB80693.1	U69174	Glycine max	calmodulin-like domain protein kinase isoenzyme gamma. CDPK gamma.
BAA13232.1	D87042	Zea mays	Calcium-dependent protein kinase.
BAA13440.1	D87707	Ipomoea batatas	calcium dependent protein kinase. CDPK.
CAA89202.1	Z49233	Chlamydomonas eugametos	calcium-stimulated protein kinase.
AAB70706.1	U82087	Tortula ruralis	calmodulin-like domain protein kinase. TrCPK1.
AAD28192.2	AF115406	Solanum tuberosum	calcium-dependent protein kinase. CDPK; catalytic domain.
AAC49405.1	U08140	Vigna radiata	calcium dependent protein kinase. CDPK.
BAA12338.1	D84408	Zea mays	calcium dependent protein kinase. ZmCDPK1.
CAA65500.1	X96723	Medicago sativa	protein kinase. CDPK.

BAA85396.1	AP000615	Oryza sativa	ESTs C22369(C12239),C22370(C12239), AU057852(S21844),AU057853(S21844) correspond to a region of the predicted gene.; similar to calcium dependent protein kinase. (AF048691).
AAA33443.1	L15390	Zea mays	calcium-dependent protein kinase. CDPK.
AAB80692.1	U69173	Glycine max	calmodulin-like domain protein kinase isoenzyme beta. CDPK beta.
CAA57156.1	X81393	Oryza sativa	calcium-dependent protein kinase. OSCPKII.
AAC05270.1	AF048691	Oryza sativa	calcium dependent protein kinase. CDPK12.
AAK26164.1	AY027885	Cucumis sativus	calcium-dependent calmodulin-independent protein kinase 5. CDPK5. CsCDPK5.
AAG46110.1	AC073166	Oryza sativa	calcium-dependent protein kinase. OSJNBb0064P21.2.
BAA02698.1	D13436	Oryza sativa	calcium-dependent protein kinase. spk.
BAA90814.1	AP001168	Oryza sativa	ESTs AU030197(E50746),AU030196(E50746) correspond to a region of the predicted gene.; Similar to calcium-dependent calmodulin-independent protein kinase CDPK (U90262).
AAF19401.1	AF203479	Glycine max	phosphoenolpyruvate carboxylase kinase. protein kinase; member of Ca ²⁺ /CaM kinase family; lacks the autoinhibitory region and EF hands.
CAB46228.1	Y18055	Arachis hypogaea	calcium dependent protein kinase. CDPK.
AAF19403.1	AF203481	Lycopersicon esculentum	phosphoenolpyruvate carboxylase kinase. protein kinase; member of Ca ²⁺ /CaM kinase family; lacks the autoinhibitory region and EF hands.
AAF19402.1	AF203480	Lycopersicon esculentum	phosphoenolpyruvate carboxylase kinase. protein kinase; member of Ca ²⁺ /CaM kinase family; lacks the autoinhibitory region and EF hands.
SEQ ID NO: 892			
AAF20931.1	AF206721	Brassica juncea	ascorbate oxidase.
BAA07734.1	D43624	Nicotiana tabacum	ascorbate oxidase precursor.
AAA33119.1	J04494	Cucumis sativus	ascorbate oxidase precursor (EC 1.10.3.3).
CAA75577.1	Y15295	Medicago truncatula	L-ascorbate oxidase. MtN23.
AAF35911.2	AF233594	Cucumis melo	ascorbate oxidase AO4. multicopper oxidase.

CAA39300.1	X55779	Cucurbita sp.	ascorbate oxidase.
BAA09528.1	D55677	Cucurbita maxima	ascorbate oxidase. AAO.
AAF35910.1	AF233593	Cucumis melo	ascorbate oxidase AO1. multicopper oxidase.
CAA71275.1	Y10226	Cucumis melo	L-ascorbate oxidase. ao3.
AAF20932.1	AF206722	Brassica juncea	ascorbate oxidase.
AAF20933.1	AF206723	Brassica juncea	ascorbate oxidase.
CAA71273.1	Y10224	Cucumis melo	L-ascorbate oxidase. ao1.
CAA71274.1	Y10225	Cucumis melo	L-ascorbate oxidase. ao1.
BAA20520.1	AB004799	Oryza sativa	ascorbate oxidase.
AAF33751.1	AF202460	Capsicum annuum	ascorbic acid oxidase.
AAB17193.1	U73105	Liriodendron tulipifera	monolignol polymerization; lignin biosynthesis. laccase. LAC2-3. diphenol oxidase; blue copper oxidase.
AAB17191.1	U73103	Liriodendron tulipifera	monolignol polymerization; lignin biosynthesis. laccase. LAC2-1. diphenol oxidase; blue copper oxidase.
AAC49536.1	U43542	Nicotiana tabacum	diphenol oxidase. laccase.
AAB17194.1	U73106	Liriodendron tulipifera	monolignol polymerization; lignin biosynthesis. laccase. LAC2-4. diphenol oxidase; blue copper oxidase.
AAB17192.1	U73104	Liriodendron tulipifera	monolignol polymerization; lignin biosynthesis. laccase. LAC2-2. diphenol oxidase; blue copper oxidase.
AAC04576.1	AF047697	Oryza sativa	p-diphenol oxidase. putative high-pI laccase.
AAB09228.1	U12757	Acer pseudoplatanus	monolignol polymerization; lignin biosynthesis. laccase. diphenol oxidase.
CAA45554.1	X64257	Brassica napus	Bp10. protein homologous to ascorbate oxidase.
AAC49538.1	U45243	Nicotiana tabacum	diphenol oxidase. laccase.

AAC49537.1	U43543	Nicotiana tabacum	diphenol oxidase. laccase.
AAD02557.1	AF049931	Petunia x hybrida	PGPS/NH15. PGPS/NH15. ascorbate oxidase homolog.
SEQ ID NO: 894			
CAB43505.1	AJ239051	Cicer arietinum	cytochrome P450. cyp81E2.
BAA74465.1	AB022732	Glycyrrhiza echinata	cytochrome P450. CYP Ge-31.
BAA93634.1	AB025016	Lotus japonicus	cytochrome P450.
BAA22422.1	AB001379	Glycyrrhiza echinata	cytochrome P450. CYP81E1.
CAA04117.1	AJ000478	Helianthus tuberosus	fatty acid in-chain hydroxylase. cytochrome P450. CYP81B11. chimeric sequence (from 5'-race).
CAB41490.1	AJ238439	Cicer arietinum	cytochrome P450 monooxygenase. cyp81E3v2.
CAA04116.1	AJ000477	Helianthus tuberosus	fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1c.
CAA10067.1	AJ012581	Cicer arietinum	cytochrome P450. cyp81E3.
AAK38079.1	AF321855	Lolium rigidum	putative cytochrome P450.
AAK38080.1	AF321856	Lolium rigidum	putative cytochrome P450.
AAK38081.1	AF321857	Lolium rigidum	putative cytochrome P450.
AAD56282.1	AF155332	Petunia x hybrida	flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.
AAC34853.1	AF082028	Hemerocallis hybrid cultivar	putative cyt P450-containing fatty acid hydroxylase. senescence-associated protein 3. SA3. mRNA accumulates in senescing petals.
AAG09208.1	AF175278	Pisum sativum	wound-inducible P450 hydroxylase. CYP82A1.
BAA12159.1	D83968	Glycine max	Cytochrome P-450 (CYP93A1).
CAA71515.1	Y10491	Glycine max	putative cytochrome P450.
CAA71876.1	Y10982	Glycine max	putative cytochrome P450.
CAA65580.1	X96784	Nicotiana tabacum	cytochrome P450. hsr515.

AAC49188.2	U29333	<i>Pisum sativum</i> cytochrome P450 monooxygenase. CYP82. new cytochrome P450 family.
AAG44132.1	AF218296	<i>Pisum sativum</i> cytochrome P450. P450 isolog.
CAA71516.1	Y10492	<i>Glycine max</i> putative cytochrome P450.
CAA64635.1	X95342	<i>Nicotiana tabacum</i> cytochrome P450. hsr515. hypersensitivity-related gene.
AAC39454.1	AF014802	<i>Eschscholzia californica</i> (S)-N-methylcoclaurine 3'-hydroxylase. CYP82B1. cytochrome P-450-dependent monooxygenase; methyl jasmonate-inducible cytochrome P-450-dependent, homologous to wound-inducible CYP82A1 of <i>Pisum sativum</i> GenBank Accession Number U29333.
AAB94590.1	AF022461	<i>Glycine max</i> CYP82C1p. CYP82C1. cytochrome P450 monooxygenase.
AAA32913.1	M32885	<i>Persea americana</i> cytochrome P-450LXXIA1 (cyp71A1).
CAA71877.1	Y10983	<i>Glycine max</i> putative cytochrome P450.
BAA84072.1	AB028152	<i>Torenia hybrida</i> flavone synthase II. cytochrome P450. TFNS5.
BAA13076.1	D86351	<i>Glycine max</i> cytochrome P-450 (CYP93A2).
AAG34695.1	AF313492	<i>Matthiola incana</i> putative cytochrome P450.
BAA84071.1	AB028151	<i>Antirrhinum majus</i> flavone synthase II. cytochrome P450. AFNS2.
AAC32274.1	AF081575	<i>Petunia x hybrida</i> flavonoid 3',5'-hydroxylase. Hfl. P450 enzyme.
BAA35080.1	AB015762	<i>Nicotiana tabacum</i> putative cytochrome P450. CYP82E1.
CAA50155.1	X70824	<i>Solanum melongena</i> flavonoid hydroxylase (P450). CYP75.
CAA70575.1	Y09423	<i>Nepeta racemosa</i> cytochrome P450. CYP71A5.
BAA92894.1	AB006790	<i>Petunia x hybrida</i> cytochrome P450. IMT-2.
CAA71513.1	Y10489	<i>Glycine max</i> putative cytochrome P450.
AAB94587.1	AF022458	<i>Glycine max</i> CYP98A2p. CYP98A2. cytochrome P450 monooxygenase.
SEQ ID NO: 895		

BAA78764.1	AB023482	Oryza sativa	ESTs C98382(C2985),D22444(C11129) correspond to a region of the predicted gene.; Similar to Arabidopsis thaliana APK1 gene for protein tyrosine-serine-threonine kinase.(D12522).
AAF43496.1	AF131222	Lophopyrum elongatum	protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.
AAK11674.1	AF339747	Lophopyrum elongatum	protein kinase. ESI47.
AAG16628.1	AY007545	Brassica napus	protein serine/threonine kinase BNK1.
BAA94510.1	AB041504	Populus nigra	protein kinase 2. PnPK2.
BAA94509.1	AB041503	Populus nigra	protein kinase 1. PnPK1.
BAA87853.1	AP000816	Oryza sativa	EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
BAB07999.1	AP002525	Oryza sativa	putative protein kinase. P0462H08.22. contains EST C22619(S11214).
BAB03429.1	AP002817	Oryza sativa	EST C22619(S11214) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).
BAB16871.1	AP002537	Oryza sativa	putative protein kinase APK1AArabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).
BAB39409.1	AP002901	Oryza sativa	putative protein kinase. P0456F08.9. contains EST C23560(R0290).
AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.
BAB21240.1	AP002953	Oryza sativa	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
AAK21965.1	AY028699	Brassica napus	receptor protein kinase PERK1.
AAG59657.1	AC084319	Oryza sativa	putative protein kinase. OSJNBa0004B24.20.
AAG03090.1	AC073405	Oryza sativa	Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).
CAB51834.1	00069	Oryza sativa	11332.5. contains eukaryotic protein kinase domain PF.

AAC61805.1	U28007	Lycopersicon esculentum	serine/threonine protein kinase. Pto kinase interactor 1. Pti1. Pti1 kinase.
AAF91336.1	AF249317	Glycine max	Pti1 kinase-like protein. Pti1a. protein kinase.
AAF91337.1	AF249318	Glycine max	Pti1 kinase-like protein. Pti1b. protein kinase.
BAB21241.1	AP002953	Oryza sativa	Putative Pto kinase interactor 1. P0426D06.21. contains ESTs AU108280(E0721),D48017(S13927).
AAB09771.1	U67422	Zea mays	CRINKLY4 precursor. cr4. receptor kinase homolog.
CAA97692.1	Z73295	Catharanthus roseus	receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
BAA92221.1	AP001278	Oryza sativa	Similar to Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).
BAA87852.1	AP000816	Oryza sativa	Similar to putative Ser/Thr protein kinase. (AC004218).
AAB61708.1	U93048	Daucus carota	somatic embryogenesis receptor-like kinase. SERK.
AAG25966.1	AF302082	Nicotiana tabacum	cytokinin-regulated kinase 1. CRK1. protein kinase; transcript abundance decreases rapidly after cytokinin treatment.
BAA90808.1	AP001168	Oryza sativa	Similar to putative receptor-like protein kinase (AL035679).
AAF76313.1	AF220603	Lycopersicon esculentum	Pto kinase. LescPth5.
AAB47421.1	U59316	Lycopersicon esculentum	serine/threonine protein kinase Pto. pto. allele of Pto bacterial speck disease resistance gene in tomato.
AAC23542.1	U20948	Ipomoea trifida	receptor protein kinase. IRK1.
BAB19337.1	AP003044	Oryza sativa	putative protein kinase. P0038C05.10. contains ESTs AU056335(S20481),AU056336(S20481).
AAC27894.1	AF023164	Zea mays	leucine-rich repeat transmembrane protein kinase 1. ltk1.
AAF66615.1	AF142596	Nicotiana tabacum	LRR receptor-like protein kinase.
CAB51480.1	Y14600	Sorghum bicolor	putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.

BAA92954.1	AP001551	Oryza sativa	Similar to Oryza sativa protein kinase (OSPK10) mRNA. (L27821).
BAA92953.1	AP001551	Oryza sativa	Similar to Arabidopsis thaliana chromosome 4 BAC clone F10M6 ; S-receptor kinase -like protein. (AL021811).
AAK11566.1	AF318490	Lycopersicon hirsutum	Pto-like protein kinase E. LhirPtoE. confers resistance to bacterial speck disease.
AAK11567.1	AF318491	Lycopersicon hirsutum	Pto-like protein kinase F. LhirPtoF.
BAA82556.1	AB030083	Populus nigra	lectin-like protein kinase. PnLPK.
CAA67145.1	X98520	Brassica oleracea	receptor-like kinase. SFR2.
SEQ ID NO: 899			
AAF61647.1	AF190634	Nicotiana tabacum	UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.
BAA89009.1	AB027455	Petunia x hybrida	anthocyanin 5-O-glucosyltransferase. PH1.
AAA59054.1	L34847	Zea mays	conjugation of the growth hormone indole-3-acetic acid (IAA). IAA-glu synthetase. iaglu.
BAA93039.1	AB033758	Citrus unshiu	limonoid UDP-glucosyltransferase. LGTase.
BAA36423.1	AB013598	Verbena x hybrida	UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.
BAA36421.1	AB013596	Perilla frutescens	UDP-glucose:anthocynin 5-O-glucosyltransferase. PF3R4.
AAF98390.1	AF287143	Brassica napus	catalyzes the transfer of glucose from UDP-glucose to sinapate and some other hydroxycinnamates (4-coumarate, caffeate, ferulate). UDP-glucose:sinapate glucosyltransferase. SGT1. SGT.
BAA36422.1	AB013597	Perilla frutescens	UDP-glucose:anthocyanin 5-O-glucosyltransferase homologue. PF3R6.
BAB07962.1	AP002524	Oryza sativa	putative anthocyanin 5-O-glucosyltransferase. P0406H10.16. contains ESTs AU067881(C10481),AU067882(C10481).
AAK16175.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.15.
AAK16181.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.16.
AAK16178.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.5.
AAG25643.1	AF303396	Phaseolus vulgaris	UDP-glucosyltransferase HRA25. putative; defense associated.

AAK16172.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.14.
BAA83484.1	AB031274	Scutellaria baicalensis	UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.
AAB36652.1	U32643	Nicotiana tabacum	immediate-early salicylate-induced glucosyltransferase. IS10a.
AAK28304.1	AF346432	Nicotiana tabacum	phenylpropanoid:glucosyltransferase 2. togt2. glucosyltransferase.
AAD21086.1	AF127218	Forsythia x intermedia	adds glucose residue to position 3 of flavonoid compounds. flavonoid 3-O-glucosyltransferase. UFGT.
AAB36653.1	U32644	Nicotiana tabacum	immediate-early salicylate-induced glucosyltransferase. IS5a.
BAA12737.1	D85186	Gentiana triflora	UDP-glucose:flavonoid-3-glucosyltransferase.
AAK28303.1	AF346431	Nicotiana tabacum	phenylpropanoid:glucosyltransferase 1. togt1. glucosyltransferase.
AAF17077.1	AF199453	Sorghum bicolor	UDP-glucose glucosyltransferase. UDP-glucose:p-hydroxymandelonitrile-o-glucosyltransferase.
AAK16180.1	AC079887	Oryza sativa	putative glucosyltransferase. OSJNBa0040E01.21.
CAA59450.1	X85138	Lycopersicon esculentum	twil. homologous to glucosyltransferases.
BAB41017.1	AB047090	Vitis labrusca x Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT1. The gene was derived from one of the parents V. labruscana cv. Ishiharawase.
BAB41026.1	AB047099	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT2.
BAB41024.1	AB047097	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT2.
BAB41022.1	AB047095	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT2.
BAB41020.1	AB047093	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT2.
BAA89008.1	AB027454	Petunia x hybrida	anthocyanidin 3-O-glucosyltransferase. PGT8.
BAB41018.1	AB047091	Vitis labrusca x Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. KyUFGT2. The gene originated in one of the parents V. vinifera cv. Centennial.
CAB56231.1	Y18871	Dorotheanthus bellidiformis	betanidin-5-O-glucosyltransferase.

AAB81683.1	AF000372	Vitis vinifera	UDP glucose:flavonoid 3-o-glucosyltransferase.
BAB41019.1	AB047092	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. ItUFGT1.
BAB41025.1	AB047098	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. FIUFGT1.
BAB41023.1	AB047096	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. AIUFGT1.
BAB41021.1	AB047094	Vitis vinifera	UDP-glucose:flavonoid 3-O-glucosyltransferase. RuUFGT1.
AAB81682.1	AF000371	Vitis vinifera	UDP glucose:flavonoid 3-o-glucosyltransferase.
BAA19659.1	AB002818	Perilla frutescens	flavonoid 3-O-glucosyltransferase. UDP glucose.
BAA90787.1	AB038248	Ipomoea batatas	UDP glucose: flavonoid 3-O-glucosyltransferase. uf3gt.
AAD04166.1	AF101972	Phaseolus lunatus	catalyzes formation of O-glucosylzeatin from zeatin and UDPG; catalyzes formation of O-xylosylzeatin from zeatin and UDPX. zeatin O-glucosyltransferase. ZOG1. cytokinin O-glucosyltransferase.
AAB86473.1	AF028237	Ipomoea purpurea	UDP glucose: flavonoid 3-O-glucosyltransferase. UF3GT-FL1.
SEQ ID NO: 900			
AAA33975.1	M11395	Glycine max	small heat shock protein.
CAA41547.1	X58711	Medicago sativa	heat shock protein.
AAB03893.1	M11318	Glycine max	17.5 kd heat shock protein Gmhsp17.6L.
AAA33672.1	M33899	Pisum sativum	18.1 kDa heat shock protein (hsp18.1).
CAA25578.1	X01104	Glycine max	heat shock protein 6871 (aa 1-153).
CAB55634.2	AJ237596	Helianthus annuus	17.9 kDa heat-shock protein. hsp17.9.
BAA33062.1	AB017273	Cuscuta japonica	low-molecular-weight heat shock protein. CJHSP17.
AAA33974.1	M11317	Glycine max	17.6 kd heat shock protein Gmhsp17.6L.
AAD30454.1	AF123257	Lycopersicon esculentum	17.6 kD class I small heat shock protein. HSP17.6.
AAD30452.1	AF123255	Lycopersicon esculentum	17.7 kD class I small heat shock protein. HSP17.7.

CAA39603.1	X56138	Lycopersicon esculentum	small heat shock protein (class I).
AAD30453.1	AF123256	Lycopersicon esculentum	17.8 kD class I small heat shock protein. HSP17.8.
CAA37847.1	X53851	Daucus carota	heat shock protein.
AAA33671.1	M33900	Pisum sativum	17.9 kDa heat shock protein (hsp17.9).
AAF34133.1	AF161179	Malus x domestica	low molecular weight heat shock protein. Hsp1.
CAA41546.1	X58710	Medicago sativa	heat shock protein.
AAB63310.1	U46544	Helianthus annuus	18.6 kDa heat-shock protein. Class I low-molecular-weight heat-shock protein.
AAB63311.1	U46545	Helianthus annuus	17.7 kDa heat shock protein. Class I low-molecular-weight heat-shock protein.
CAB08441.1	Z95153	Helianthus annuus	17.6 kD class I small heat-shock protein HSP17.6. Ha hsp17.6.
CAA42222.1	X59701	Helianthus annuus	17.6 kDa heat shock protein.
AAC39360.1	U63631	Fragaria x ananassa	LMW heat shock protein.
AAA33910.1	M80939	Oryza sativa	16.9 kDa heat shock protein.
CAA37848.1	X53852	Daucus carota	heat shock protein.
AAA33909.1	M80938	Oryza sativa	16.9 kDa heat shock protein.
CAA43210.1	X60820	Oryza sativa	16.9 KD low molecular weight heat shock protein.
CAA37864.1	X53870	Chenopodium rubrum	heat-shock protein.
AAD49336.1	AF166277	Nicotiana tabacum	low molecular weight heat-shock protein. LHS-1. TLHS-1.
AAA61632.1	U08601	Papaver somniferum	low molecular weight heat-shock protein.
AAB72109.1	AF022217	Brassica rapa	low molecular weight heat-shock protein. BcHSP17.6. 17.6 kDa; cytosolic class I.
CAA63902.1	X94192	Pennisetum glaucum	heat shock protein 16.9. hsp16.9.
AAB39856.1	U81385	Oryza sativa	heat shock protein. Oshsp16.9C. class I, low molecular mass.

CAA46641.1	X65725	Zea mays	heat shock protein 17.2. Zmhsp 17.2. Class I low molecular weight heat shock protein.
CAA08908.1	AJ009880	Castanea sativa	molecular chaperone. cytosolic class I small heat-shock protein HSP17.5. hsp17.5.
CAB93512.1	AJ243565	Brassica oleracea	putative class I small heat shock protein. HSP17.7-a protein. hsp17.7-a.
CAA63903.1	X94193	Pennisetum glaucum	heat shock protein 17.9. hsp17.9.
CAB36910.1	AJ000691	Quercus suber	stress protein chaperone. heat shock protein 17.4. hsp17.
CAA63901.1	X94191	Pennisetum glaucum	heat shock protein 17.0. hsp17.0.
AAC78392.1	U83669	Oryza sativa	low molecular mass heat shock protein Oshsp17.3. OSHSP17.3. class I LMMHSP.
BAA02160.1	D12635	Oryza sativa	'low molecular weight heat shock protein'.
AAC78393.1	U83670	Oryza sativa	low molecular mass heat shock protein Oshsp18.0. OSHSP18.0. class I LMMHSP.
CAA31785.1	X13431	Triticum aestivum	put. heat shock protein (AA 1 -151).
CAA63570.1	X92983	Pseudotsuga menziesii	low molecular weight heat-shock protein.
AAC78394.1	U83671	Oryza sativa	low molecular mass heat shock protein Oshsp17.7. OSHSP17.7. class I LMMHSP.
CAA63571.1	X92984	Pseudotsuga menziesii	low molecular weight heat-shock protein.

SEQ ID NO: 901

AAG08959.1	AF122051	Solanum tuberosum	tuber-specific and sucrose-responsive element binding factor. TSF. R2R3 MYB class transcription factor.
AAG08960.1	AF122052	Solanum tuberosum	tuber-specific and sucrose-responsive element binding factor. TSF. R2R3 MYB class transcription factor.
AAG08961.1	AF122053	Solanum tuberosum	tuber-specific and sucrose-responsive element binding factor. TSF. R2R3 MYB class transcription factor.
AAF67053.1	AF190304	Adiantum raddianum	c-myb-like transcription factor. MYB3R-1. contains three MYB repeats.
AAF67052.1	AF190303	Adiantum raddianum	c-myb-like transcription factor. MYB3R-1. contains three MYB repeats.
AAF34434.1	AF172282	Oryza sativa	myb-like protein. DUPR11.29.

AAF78888.1	AF189786	Physcomitrella patens putative c-myb-like transcription factor. MYB3R-1. PpMYB3R-1.
AAF78887.1	AF189785	Physcomitrella patens putative c-myb-like transcription factor. MYB3R-1. PpMYB3R-1.
AAF43043.1	AF236059	Papaver rhoeas putative Myb-related domain. pmr.
BAA94769.1	AP001859	Oryza sativa Similar to Arabidopsis thaliana chromosome 4, BAC clone F4D11; putative myb-protein. (AL022537).
AAF78890.1	AF189788	Hordeum vulgare putative c-myb-like transcription factor. MYB3R-1. HvMYB3R-1.
AAF78889.1	AF189787	Hordeum vulgare putative c-myb-like transcription factor. MYB3R-1. HvMYB3R-1.
BAA88169.1	AP000836	Oryza sativa Similar to putative transcription factor (AF062890).
BAA88205.1	AP000837	Oryza sativa Similar to putative transcription factor (AF062890).
CAA78388.1	Z13998	Petunia x hybrida DNA-binding protein; transcriptional activator. protein 3. myb.Ph3. related to animal myb proto-oncoproteins.
AAF67051.1	AF190302	Secale cereale c-myb-like transcription factor. MYB3R-1. contains three MYB repeats.
AAF67050.1	AF190301	Secale cereale c-myb-like transcription factor. MYB3R-1. contains three MYB repeats.
AAG28525.1	AF198498	Nicotiana tabacum anther-specific myb-related protein 2. mybAS2. NtMYBAS2; contains tandem R2, R3 myb domains similar to c-myb family.
BAB12688.1	AP002746	Oryza sativa putative MYB family transcription factor. P0671B11.3. contains ESTs AU082307(E0784),C72014(E0784).
BAA99440.1	AP002743	Oryza sativa putative MYB family transcription factor. P0710E05.27. contains ESTs AU082307(E0784),C72014(E0784).
AAK19619.1	AF336286	Gossypium hirsutum GHMYB9. ghmyb9. similar to myb.
CAA64615.1	X95297	Lycopersicon esculentum transcription factor. THM1. myb-related.
BAA81730.1	AB029159	Glycine max GmMYB29A1.
CAA50224.1	X70879	Hordeum vulgare MybHv1. myb1.
CAA50222.1	X70877	Hordeum vulgare MybHv1. myb1.

CAB40189.1	AJ133638	Avena sativa	transcriptional activator. myb protein. gamyb.
AAG28526.1	AF198499	Nicotiana tabacum	anther-specific myb-related protein 1. mybAS1. NtMYBAS1; contains N-terminal R2, R3 myb domain repeats similar to c-myb.
AAD31395.1	AF114162	Lolium temulentum	gibberellin MYB transcription factor. GAMyb. R2/R3-MYB.
BAA81732.1	AB029161	Glycine max	GmMYB29A2.
BAA81731.1	AB029160	Glycine max	GmMYB29A1.
CAA61021.1	X87690	Hordeum vulgare	transcriptional activator of alpha-amylase gene promoter. GAMyb protein. Gam1.
AAG22863.1	AY008692	Hordeum vulgare	transcription factor GAMyb. Gamyb.
BAA96421.1	AB044084	Triticum aestivum	transcription activator for gibberellin response. GAMyb protein. Ta-GAMyb.
BAA81733.2	AB029162	Glycine max	GmMYB29A2.
BAA81736.1	AB029165	Glycine max	GmMYB29B2.
AAA33067.1	L04497	Gossypium hirsutum	MYB A; putative.
BAB39972.1	AP003018	Oryza sativa	putative transcription factor (myb). OSJNBa0004B13.27. contains ESTs AU097474(S5087),D40175(S1959).
CAA72218.1	Y11415	Oryza sativa	myb.
CAA67000.1	X98355	Oryza sativa	activator of alpha-amylase gene promoter. transcription factor GAMyb. Gam1. Myb-like; expression is regulated by gibberellin.
BAB39987.1	AP003020	Oryza sativa	putative transcription factor (myb). P0498A12.16. contains ESTs AU097474(S5087),D40175(S1959).
CAA78387.1	Z13997	Petunia x hybrida	DNA-binding protein, transcriptional activator. protein 2. myb.Ph2. related to animal myb proto-oncoproteins.
CAA72217.1	Y11414	Oryza sativa	myb.
BAA23341.1	D88621	Oryza sativa	transfactor. OSMYB5. Osmyb5.

BAA93038.1	AP001552	Oryza sativa	EST AU082058(C12976) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana putative transcription factor (AF062916).
CAA64614.1	X95296	Lycopersicon esculentum	transcription factor. THM27. myb-related.
AAK19616.1	AF336283	Gossypium hirsutum	GHMYB25. ghmyb25. similar to myb; contains an unspliced intron.
CAA78386.1	Z13996	Petunia x hybrida	DNA binding protein; transcriptional activator. protein 1. myb.Ph3. Product related to animal myb proto-oncoproteins. Sequence from nucleotide 992 is not included in clone cPF1 and has been obtained by PCR amplification of cDNA.
CAA67575.1	X99134	Lycopersicon esculentum	transcription factor. THM6. myb-related.
BAA88222.1	AB028650	Nicotiana tabacum	myb-related transcription factor LBM2. lbm2.
SEQ ID NO: 902			
CAA57773.1	X82329	Arachis hypogaea	chitinase (class II). chi2;1.
AAD54935.1	AF141373	Petroselinum crispum	random hydrolysis of 1,4-beta-acetamido-2-deoxy-D-glucoside linkages in chitin. chitinase precursor. Chi2-1. class II.
AAD54936.1	AF141374	Petroselinum crispum	random hydrolysis of 1,4-beta-acetamido-2-deoxy-D-glucoside linkages in chitin. chitinase precursor. Chi2-2. class II.
AAF00131.1	AF147091	Fragaria x ananassa	chitin degradation. class II chitinase. Chi2-1.
AAC95376.1	AF105426	Cynodon dactylon	chitinase. Cht2.
BAA95846.1	AP002070	Oryza sativa	Similar to Oryza sativa clone RGCH7 chitinase. (AF013581).
AAA32986.1	M95835	Brassica napus	endochitinase. Ch25.
AAF69783.1	AF135143	Arabis lemmonii	class I chitinase.
AAF69775.1	AF135135	Arabis drummondii	class I chitinase.
AAF69792.1	AF135152	Arabis parishii	class I chitinase.
AAC95375.1	AF105425	Cynodon dactylon	chitinase. Cht1.
AAF69785.1	AF135145	Arabis lignifera	class I chitinase.

AAF69770.1	AF135130	<i>Arabis holboellii</i> class I chitinase.
AAF69781.1	AF135141	<i>Arabis gunnisoniana</i> class I chitinase.
AAF69777.1	AF135137	<i>Arabis fecunda</i> class I chitinase.
AAF69790.1	AF135150	<i>Arabis microphylla</i> class I chitinase.
AAF69787.1	AF135147	<i>Arabis lignifera</i> class I chitinase.
AAF69772.1	AF135132	<i>Arabis gunnisoniana</i> class I chitinase.
AAF69782.1	AF135142	<i>Halimolobos perplexa</i> var. <i>perplexa</i> class I chitinase.
AAF69784.1	AF135144	<i>Arabis lemmonii</i> class I chitinase.
AAF69788.1	AF135148	<i>Arabis lyallii</i> class I chitinase.
BAA03750.1	D16222	<i>Oryza sativa</i> endochitinase. Cht-2.
AAF69776.1	AF135136	<i>Arabis fecunda</i> class I chitinase.
CAA40107.1	X56787	<i>Oryza sativa</i> chitinase.
BAB13369.1	AB048531	<i>Psophocarpus tetragonolobus</i> class I chitinase.
AAF69778.1	AF135138	<i>Arabis glabra</i> class I chitinase.
AAF69786.1	AF135146	<i>Arabis lignifera</i> class I chitinase.
BAA82826.1	AB023464	<i>Arabis gemmifera</i> basic endochitinase. ChiB.
AAF69773.1	AF135133	<i>Arabis blepharophylla</i> class I chitinase.
AAF69791.1	AF135151	<i>Arabis microphylla</i> class I chitinase.
AAF69793.1	AF135153	<i>Arabis parishii</i> class I chitinase.
CAA39535.1	X56063	<i>Oryza sativa</i> chitinase.
BAA03749.1	D16221	<i>Oryza sativa</i> endochitinase. Cht-1.

AAF69789.1	AF135149	Arabis microphylla	class I chitinase.
CAA71402.1	Y10373	Medicago truncatula	chitinase.
AAC16010.1	AF061805	Elaeagnus umbellata	acidic chitinase.
CAA53626.1	X76041	Triticum aestivum	endochitinase. CHI.
BAA33971.1	AB008892	Nicotiana tabacum	chitinase 134. Chn134.
CAA47921.1	X67693	Solanum tuberosum	chitinase. SK2. endochitinase.
AAF69780.1	AF135140	Arabis glabra	class I chitinase.
BAB18519.1	AB051578	Secale cereale	seed chitinase-a. rsca.
AAA51377.1	L37289	Oryza sativa	chitinolytic activity, antifungal activity. chitinase.
AAB41324.1	U83591	Medicago sativa	class I chitinase.
CAC17793.1	AJ301671	Nicotiana sylvestris	hydrolysis of chitin. endochitinase. chnb. class I chitinase.
AAB41325.1	U83592	Medicago sativa	class I chitinase.
AAB23263.1	S43926	Phaseolus vulgaris	chitinase. CH5B. This sequence comes from Fig. 1.
AAA33756.1	M13968	Phaseolus vulgaris	chitinase (EC 3.2.1.14).
CAA35945.1	X51599	Nicotiana tabacum	chitinase. CHN50.
AAA34070.1	M15173	Nicotiana tabacum	endochitinase precursor (EC 3.2.1.14).
CAA45822.1	X64519	Nicotiana tabacum	chitinase B class I. CHN200.

SEQ ID NO: 903

BAA78764.1	AB023482	Oryza sativa	ESTs C98382(C2985),D22444(C11129) correspond to a region of the predicted gene.; Similar to Arabidopsis thaliana APK1 gene for protein tyrosine-serine-threonine kinase.(D12522).
AAF43496.1	AF131222	Lophopyrum elongatum	protein serine/threonine kinase. ESI47. induced in roots by salt stress, osmotic stress, and ABA treatment.
AAK11674.1	AF339747	Lophopyrum elongatum	protein kinase. ESI47.

AAG16628.1	AY007545	Brassica napus	protein serine/threonine kinase BNK1.
BAA94509.1	AB041503	Populus nigra	protein kinase 1. PnPK1.
BAA87853.1	AP000816	Oryza sativa	EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
BAA94510.1	AB041504	Populus nigra	protein kinase 2. PnPK2.
BAB16871.1	AP002537	Oryza sativa	putative protein kinase APK1A Arabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192), D25110(R3192).
BAB03429.1	AP002817	Oryza sativa	EST C22619(S11214) corresponds to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 2, BAC clone T17D12; putative protein kinase (AC006587).
BAB07999.1	AP002525	Oryza sativa	putative protein kinase. P0462H08.22. contains EST C22619(S11214).
BAB39409.1	AP002901	Oryza sativa	putative protein kinase. P0456F08.9. contains EST C23560(R0290).
BAB21240.1	AP002953	Oryza sativa	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461), C22360(C11461).
AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.
CAB51834.1	00069	Oryza sativa	l1332.5. contains eukaryotic protein kinase domain PF.
BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808), AU056702(S20808).
AAK21965.1	AY028699	Brassica napus	receptor protein kinase PERK1.
AAG03090.1	AC073405	Oryza sativa	Similar to an Arabidopsis somatic embryogenesis receptor-like kinase (AC007504).
BAB19337.1	AP003044	Oryza sativa	putative protein kinase. P0038C05.10. contains ESTs AU056335(S20481), AU056336(S20481).
BAA90808.1	AP001168	Oryza sativa	Similar to putative receptor-like protein kinase (AL035679).
AAG59657.1	AC084319	Oryza sativa	putative protein kinase. OSJNBa0004B24.20.
AAB47424.1	U59317	Lycopersicon pimpinellifolium	serine/threonine protein kinase Fen. Fen. fenthion sensitivity gene from tomato.

AAC48932.1	U13923	<i>Lycopersicon pimpinellifolium</i> Fen. putative serine/threonine protein kinase; similar to product encoded by <i>Lycopersicon pimpinellifolium</i> Pto gene, GenBank Accession Number U02271; Fen is a member of the Pto gene family.
AAF76307.1	AF220602	<i>Lycopersicon pimpinellifolium</i> Fen kinase.
BAA92221.1	AP001278	<i>Oryza sativa</i> Similar to <i>Arabidopsis thaliana</i> chromosome II BAC F12L6 genomic sequence, putative protein kinase. (AC004218).
BAA87852.1	AP000816	<i>Oryza sativa</i> Similar to putative Ser/Thr protein kinase. (AC004218).
AAB61708.1	U93048	<i>Daucus carota</i> somatic embryogenesis receptor-like kinase. SERK.
AAK11566.1	AF318490	<i>Lycopersicon hirsutum</i> Pto-like protein kinase E. LhirPtoE. confers resistance to bacterial speck disease.
AAK11568.1	AF318492	<i>Lycopersicon hirsutum</i> Pto-like protein kinase B. LhirPtoB.
AAD21872.1	AF078082	<i>Phaseolus vulgaris</i> receptor-like protein kinase homolog RK20-1.
AAF66615.1	AF142596	<i>Nicotiana tabacum</i> LRR receptor-like protein kinase.
AAC23542.1	U20948	<i>Ipomoea trifida</i> receptor protein kinase. IRK1.
AAF91337.1	AF249318	<i>Glycine max</i> Pti1 kinase-like protein. Pti1b. protein kinase.
AAC27894.1	AF023164	<i>Zea mays</i> leucine-rich repeat transmembrane protein kinase 1. ltk1.
AAF76314.1	AF220603	<i>Lycopersicon esculentum</i> Fen kinase. Lescfen.
AAB47422.1	U59318	<i>Lycopersicon esculentum</i> serine/threonine protein kinase Fen. fen. allele of Fen, fenthion sensitivity gene from tomato.
AAF76313.1	AF220603	<i>Lycopersicon esculentum</i> Pto kinase. LescPth5.
AAB47421.1	U59316	<i>Lycopersicon esculentum</i> serine/threonine protein kinase Pto. pto. allele of Pto bacterial speck disease resistance gene in tomato.
AAF91336.1	AF249317	<i>Glycine max</i> Pti1 kinase-like protein. Pti1a. protein kinase.
AAK11567.1	AF318491	<i>Lycopersicon hirsutum</i> Pto-like protein kinase F. LhirPtoF.
AAC61805.1	U28007	<i>Lycopersicon esculentum</i> serine/threonine protein kinase. Pto kinase interactor 1. Pti1. Pti1 kinase.

AAB93834.1	U82481	Zea mays	KI domain interacting kinase 1. KIK1. receptor-like protein kinase; serine/threonine protein kinase.
CAA97692.1	Z73295	Catharanthus roseus	receptor-like protein kinase. CRPK1. Autophosphorylation predominantly on Thr, less on Ser. Mechanism: autophosphorylation in cis.
CAA73134.1	Y12531	Brassica oleracea	serine/threonine kinase. BRLK.
AAF76306.1	AF220602	Lycopersicon pimpinellifolium	Pto kinase.
AAB47423.1	U59315	Lycopersicon pimpinellifolium	serine/threonine protein kinase Pto. Pto. bacterial speck disease resistance in tomato; disease resistance gene.
BAB21241.1	AP002953	Oryza sativa	Putative Pto kinase interactor 1. P0426D06.21. contains ESTs AU108280(E0721),D48017(S13927).
AAC48914.1	U02271	Lycopersicon pimpinellifolium	protein kinase.
SEQ ID NO: 904			
AAF65545.1	AF233894	Perilla citriodora	limonene synthase.
AAG31437.1	AF241792	Perilla frutescens	limonene synthase.
AAK06663.1	AF317695	Perilla frutescens var. frutescens	limonene synthase.
AAG31435.1	AF241790	Perilla citriodora	limonene synthase.
BAA21629.1	AB005744	Perilla frutescens	catalyzing the cyclization of geranyl pyrophosphate to 1-limonene. 1-limonene synthase. gPFLC. similar to perilla PFLC-1:DDBJ Acc#D49368.
AAG31438.1	AF241793	Perilla frutescens	limonene synthase.
BAA08367.1	D49368	Perilla frutescens	limonene cyclase.
AAC37366.1	L13459	Mentha spicata	4S-limonene synthase.
AAD50304.1	AF175323	Mentha longifolia	limonene synthase. monoterpene synthase.
AAG01140.1	AF282875	Schizonepeta tenuifolia	(+)-4R-limonene synthase.
AAF21053.1	AF212433	Capsicum annuum	UV-induced sesquiterpene cyclase. SC2.

BAA82141.1	AB023816	Solanum tuberosum	vetispiradiene synthase. PVS4. potato sesquiterpene cyclase.
AAF74977.1	AF270425	Gossypium hirsutum	(E,E)-farnesyl diphosphate cyclase. (+)-delta-cadinene synthase. cdn2. sesquiterpene cyclase.
BAA82092.1	AB022598	Solanum tuberosum	vetispiradiene synthase. PVS1. potato sesquiterpene cyclase.
BAA82109.1	AB022720	Solanum tuberosum	vetispiradiene synthase. PVS3. potato sesquiterpene cyclase; PVS3.
AAG09949.1	AF171216	Lycopersicon esculentum	vetispiradiene synthase. LEVS2. sesquiterpene cyclase.
BAA82108.1	AB022719	Solanum tuberosum	vetispiradiene synthase. PVS2. potato sesquiterpene cyclase; PVS2.
AAC12784.1	U88318	Gossypium hirsutum	(E,E)-farnesyl diphosphate cyclizing. (+)-delta-cadinene synthase. cdn1. sesquiterpene cyclase; delta-cadinene synthase.
AAK15641.1	AF326117	Capsicum annuum	sesquiterpene cyclase. PSC2.
AAC61260.1	AF061285	Capsicum annuum	sesquiterpene cyclase. UV induced.
AAG24640.2	AF304444	Artemisia annua	sesquiterpene cyclase.
CAC12731.1	AJ271792	Artemisia annua	putative sesquiterpene cyclase. cASC125.

SEQ ID NO: 905

AAF64450.1	AF239928	Euphorbia esula	glutathione S-transferase. similar to auxin-inducible GST.
AAG34803.1	AF243368	Glycine max	glutathione S-transferase GST 13.
AAG16759.1	AY007561	Lycopersicon esculentum	putative glutathione S-transferase T4.
AAG34798.1	AF243363	Glycine max	glutathione S-transferase GST 8.
AAG34797.1	AF243362	Glycine max	glutathione S-transferase GST 7.
AAG16758.1	AY007560	Lycopersicon esculentum	putative glutathione S-transferase T3.
AAG34809.1	AF243374	Glycine max	glutathione S-transferase GST 19.
AAG34801.1	AF243366	Glycine max	glutathione S-transferase GST 11.
AAG34796.1	AF243361	Glycine max	glutathione S-transferase GST 6.

AAG34807.1	AF243372	Glycine max glutathione S-transferase GST 17.
AAG16757.1	AY007559	Lycopersicon esculentum putative glutathione S-transferase T2.
AAG16756.1	AY007558	Lycopersicon esculentum putative glutathione S-transferase T1.
AAG34804.1	AF243369	Glycine max glutathione S-transferase GST 14.
AAG34810.1	AF243375	Glycine max glutathione S-transferase GST 20.
AAG34808.1	AF243373	Glycine max glutathione S-transferase GST 18.
AAG34805.1	AF243370	Glycine max glutathione S-transferase GST 15.
AAG34844.1	AF244701	Zea mays glutathione S-transferase GST 36.
AAG34829.1	AF244686	Zea mays glutathione S-transferase GST 21.
AAG34831.1	AF244688	Zea mays glutathione S-transferase GST 23.
AAA68430.1	J03679	Solanum tuberosum glutathione S-transferase. gst1. previously called pathogenesis-related protein; prp1-1.
AAC18566.1	AF048978	Glycine max 2,4-D inducible glutathione S-transferase. GSTa.
AAG34832.1	AF244689	Zea mays glutathione S-transferase GST 24.
AAG34800.1	AF243365	Glycine max glutathione S-transferase GST 10.
AAG34849.1	AF244706	Zea mays glutathione S-transferase GST 41.
AAG34837.1	AF244694	Zea mays glutathione S-transferase GST 29.
AAC32118.1	AF051214	Picea mariana probable glutathione S-transferase. Sb18. similar to Nicotiana tabacum probable glutathione S-transferase encoded by GenBank Accession Number X56266.
AAG41204.1	AF321437	Suaeda maritima glutathione transferase.
AAG34802.1	AF243367	Glycine max glutathione S-transferase GST 12.
AAF29773.1	AF159229	Gossypium hirsutum glutathione S-transferase. GST.
AAG32472.1	AF309379	Oryza sativa subsp. japonica putative glutathione S-transferase OsGSTU3.

AAG34836.1	AF244693	Zea mays	glutathione S-transferase GST 28.
CAA04391.1	AJ000923	Carica papaya	glutathione transferase. PGST1.
CAA71784.1	Y10820	Glycine max	glutathione transferase.
CAA09187.1	AJ010448	Alopecurus myosuroides	glutathione transferase. GST1a.
AAG34795.1	AF243360	Glycine max	glutathione S-transferase GST 5.
CAA09188.1	AJ010449	Alopecurus myosuroides	glutathione transferase. GST1b.
AAG34806.1	AF243371	Glycine max	glutathione S-transferase GST 16.
CAC24549.1	AJ296343	Cichorium intybus x Cichorium endivia	glutathione S-transferase. chi-GST1. auxin-induced GST.
AAC28101.1	AF079511	Mesembryanthemum crystallinum	glutathione S-transferase.
SEQ ID NO: 907			
AAA33280.1	L20475	Datura stramonium	29kDa protein; high homology to aa sequence of tropinone reductases.
AAA33281.1	L20473	Datura stramonium	catalyses a stereospecific reduction of tropinone to tropine. tropinone reductase-I.
CAC34420.1	AJ307584	Solanum tuberosum	tropine forming tropinone reductase. tropinone reductase I. TRI.
BAA85844.1	AB026544	Hyoscyamus niger	tropinone reductase-I. tr1.
BAA13547.1	D88156	Hyoscyamus niger	tropinone reductase-I.
AAA33282.1	L20474	Datura stramonium	catalyses a stereospecific reduction of tropinone to pseudotropine. tropinone reductase-II.
AAB09776.1	L20485	Hyoscyamus niger	tropinone reductase-II.
BAA85845.1	AB026545	Hyoscyamus niger	tropinone reductase-II. tr2.
CAB52307.1	AJ245634	Solanum tuberosum	pseudotropine forming tropinone reductase. tropinone reductase II. TRII.
CAC19810.1	AJ292343	Solanum tuberosum	pseudotropine forming tropinone reductase. tropinone reductase II. trII.
CAA45866.1	X64566	Cuphea lanceolata	beta-ketoacyl-ACP reductase. Clkr27. 3-oxoacyl-[acyl-carrier protein] reductase.

CAA45793.1	X64463	Brassica napus	3-oxoacyl-[acyl-carrier protein] reductase.
AAB82767.1	U89509	Zea mays	cuticular wax biosynthesis. b-keto acyl reductase. glossy8.
AAB82766.1	U89510	Hordeum vulgare	cuticular wax biosynthesis. b-keto acyl reductase. glossy8.
CAA74176.1	Y13861	Nicotiana tabacum	enoyl-ACP reductase. enr-T2.
AAB20114.2	S60064	Brassica napus	enoyl-acyl carrier protein reductase. This sequence comes from fig3; conceptual translation differs from published sequence.
CAA74177.1	Y13862	Nicotiana tabacum	enoyl-ACP reductase. enr-T1.
AAC78100.1	AF093628	Oryza sativa	protochlorophyllide reductase homolog.
CAA05879.1	AJ003124	Petunia x hybrida	enoyl-ACP reductase. pte.
CAA64729.1	X95462	Brassica napus	enoyl reductase.
CAA05816.1	AJ003025	Oryza sativa	enoyl-ACP reductase.
BAA99570.1	AB036823	Chlorella vulgaris	oxidoreductase. oxi.

SEQ ID NO: 909

BAA82107.1	AB022693	Nicotiana tabacum	transcription factor. NtWRKY1.
AAC31956.1	AF080595	Pimpinella brachycarpa	zinc finger protein. ZFP1. WRKY1.
AAD55974.1	AF121353	Petroselinum crispum	zinc-finger type transcription factor WRKY1. WRKY1.
BAA77383.1	AB020590	Nicotiana tabacum	transcription factor NtWRKY2.
AAC49527.1	U48831	Petroselinum crispum	WRKY1. contains two WRKY domains; WRKY-type DNA-binding protein; sequence-specific DNA-binding protein.
AAD32677.1	AF140554	Avena sativa	DNA-binding protein WRKY1. wrky1. putative transcription factor.
CAA88326.1	Z48429	Avena fatua	binds conserved cis-element from cereal alpha-Amy2 promoters. DNA-binding protein.
AAD16139.1	AF096299	Nicotiana tabacum	DNA-binding protein 2. WRKY2. transcription factor.
BAA86031.1	AB026890	Nicotiana tabacum	transcription factor NtWRKY4.

AAC37515.1	L44134	Cucumis sativus	SPF1-like DNA-binding protein.
AAK16171.1	AC079887	Oryza sativa	putative DNA-binding protein. OSJNBa0040E01.10.
AAF23898.1	AF193802	Oryza sativa	zinc finger transcription factor WRKY1.
AAD16138.1	AF096298	Nicotiana tabacum	DNA-binding protein 1. WRKY1. transcription factor.
AAC49529.1	U58540	Petroselinum crispum	WRKY2. Contains two WRKY domains; WRKY-type DNA-binding protein.
CAB97004.1	AJ278507	Solanum tuberosum	putative transcription factor. WRKY DNA binding protein. WRKY1.
BAB19075.1	AP002744	Oryza sativa	putative DNA-binding protein homolog. P0006C01.17.
BAB19096.1	AP002839	Oryza sativa	putative DNA-binding protein homolog. P0688A04.2.
AAK16170.1	AC079887	Oryza sativa	putative DNA binding protein. OSJNBa0040E01.4.
BAB40073.1	AP003074	Oryza sativa	putative WRKY DNA binding protein. OSJNBa0004G10.20. contains EST C26525(C12525).
AAD38283.1	AC007789	Oryza sativa	putative WRKY DNA binding protein. OSJNBa0049B20.9.
BAB18313.1	AP002865	Oryza sativa	putative WRKY DNA binding protein. P0034C11.1. contains EST C26525(C12525).
CAA88331.1	Z48431	Avena fatua	binds conserved cis-element from cereal alpha-Amy2 promoters. DNA-binding protein.
AAC49528.1	U56834	Petroselinum crispum	DNA-binding. WRKY3. WRKY-type DNA-binding protein.
AAG35658.1	AF204925	Petroselinum crispum	transcription factor WRKY4. WRKY4. binds to W box (TTGACC) elements.
BAB16432.1	AB041520	Nicotiana tabacum	WRKY transcription factor Nt-SubD48. Nt-SubD48.
AAD32676.1	AF140553	Avena sativa	DNA-binding protein WRKY3. wrky3. putative transcription factor.
AAG46150.1	AC018727	Oryza sativa	putative DNA-binding protein. OSJNBa0056G17.18.
BAA77358.1	AB020023	Nicotiana tabacum	WRKY domain Zn-finger type DNA-binding protein. DNA-binding protein NtWRKY3.
AAG35659.1	AF204926	Petroselinum crispum	transcription factor WRKY5. WRKY5. binds to W box (TTGACC) elements.
AAD27591.1	AF121354	Petroselinum crispum	binds sequence specifically to W Boxes (TTGACC). transcription factor. WRKY3. sequence specific DNA-binding protein.

CAB66338.1	AJ279697	Betula pendula wrky-type DNA binding protein. wrky.
AAF61864.1	AF193771	Nicotiana tabacum DNA-binding protein 4. WRKY4. transcription factor.
BAA87069.1	AB035271	Matricaria chamomilla elicitor-induced DNA-binding protein homolog. McWRKY1.
AAF61863.1	AF193770	Nicotiana tabacum DNA-binding protein 3. WRKY3. transcription factor.
SEQ ID NO: 910		
AAC09420.1	M68929	Mitochondrion Marchantia polymorpha rps14.
CAA33994.1	X15901	Plastid Oryza sativa ribosomal protein S14. rps14.
SEQ ID NO: 911		
CAA55128.1	X78325	Nicotiana tabacum chitinase/lysozyme. Pz.
CAA54373.1	X77110	Nicotiana tabacum chitinase, class V. chi-V.
CAA54374.1	X77111	Nicotiana tabacum chitinase, class V. chi-V.
SEQ ID NO: 912		
CAB55394.1	AL117264	Oryza sativa zwh0010.1. similar to Arabidopsis germin-like protein 6 (AF032976); Method: conceptual translation with partial peptide sequencing.
BAA78563.1	AB024338	Atriplex lentiformis germin-like protein.
AAB97470.1	AF042489	Oryza sativa germin-like protein 16. glp16.
AAA33030.1	M93041	Mesembryanthemum crystallinum germin-like protein. germin-like protein.
CAB65371.1	AJ250834	Pisum sativum germin-like protein. ger2b. 2nd variant of the clone PsGER2.
CAB55559.1	AJ237943	Triticum aestivum germin-like protein. glp2b.
CAB65370.1	AJ250833	Pisum sativum germin-like protein. ger2a. 1st variant of this clone.
CAB55558.1	AJ237942	Triticum aestivum germin-like protein. glp2a.
AAD43971.1	AF141878	Oryza sativa germin-like protein 1 precursor. RGLP1. similar to barley epidermis/papilla-specific oxalate oxidase-like protein.

AAD43973.1	AF141880	Oryza sativa	germin-like protein 1 precursor. RGLP1. similar to barley epidermis/papilla-specific oxalate oxidase-like protein.
AAC04837.1	AF032976	Oryza sativa	germin-like protein 6. GER6. similar to wheat and barley oxalate oxidase.
AAG00425.1	AF250933	Hordeum vulgare	germin A. GerA. apoplastic protein; contains prepeptide for targeting into the cell wall.
AAD43972.1	AF141879	Oryza sativa	germin-like protein 2 precursor. RGLP2. similar to barley epidermis/papilla-specific oxalate oxidase-like protein.
CAA63659.1	X93171	Hordeum vulgare	oxalate oxidase-like protein or germin-like protein.
AAC04833.1	AF032972	Oryza sativa	germin-like protein 2. GER2. similar to wheat and barley oxalate oxidase.
AAC04834.1	AF032973	Oryza sativa	germin-like protein 3. GER3. similar to wheat and barley oxalate oxidase.
AAC04832.1	AF032971	Oryza sativa	germin-like protein 1. GER1. similar to wheat and barley oxalate oxidase.
AAG00426.1	AF250934	Hordeum vulgare	germin B. GerB. apoplastic protein; contains prepeptide for targeting into the cell wall.
AAG00427.1	AF250935	Hordeum vulgare	germin F. GerF. apoplastic protein; contains prepeptide for targeting into the cell wall.
AAF34811.1	AF005084	Triticum aestivum	oxalate oxidase. up-regulated by aluminum.
AAC04835.1	AF032974	Oryza sativa	germin-like protein 4. GER4. similar to wheat and barley oxalate oxidase.
BAB39965.1	AP003018	Oryza sativa	probable germin protein 4. OSJNBa0004B13.19. contains ESTs AU101991(S4037),AU070167(R0031).
BAB39980.1	AP003020	Oryza sativa	probable germin protein 4. P0498A12.8. contains ESTs AU101991(S4037),AU070167(R0031).
AAG00428.1	AF250936	Hordeum vulgare	germin D. GerD. apoplastic protein; contains prepeptide for targeting into the cell wall.
AAA20245.1	U01963	Hordeum vulgare	germin subunit.
CAC19429.1	AJ291825	Lolium perenne	oxalate oxidase. oxO1.
AAA34270.1	M63223	Triticum aestivum	germin. germin 9f-2.8.
AAA34268.1	M21962	Triticum aestivum	germin protein precursor.

CAA74595.1	Y14203	Hordeum vulgare	oxalate oxidase.
AAG00429.1	AF250937	Hordeum vulgare	germin E. GerE. apoplastic protein.
CAB65369.1	AJ250832	Pisum sativum	germin-like protein. ger1.
AAA32959.1	L15737	Hordeum vulgare	oxalate oxidase. This is the sequence of the complete mature peptide.
CAA71052.1	Y09917	Triticum aestivum	germin homolog. pSBGer3.
AAA34271.1	M63224	Triticum aestivum	germin. germin 9f-3.8.
CAA71050.1	Y09915	Triticum aestivum	germin homolog. pSBGer1.
BAB18339.1	AP002865	Oryza sativa	putative germin protein. P0034C11.30. contains EST C97263(C53484).
AAD38298.1	AC007789	Oryza sativa	putative oxalate oxidase (germin protein). OSJNBa0049B20.25.
BAA86880.1	AB028454	Barbula unguiculata	germin-like protein.
AAF03355.1	AF132671	Nicotiana plumbaginifolia	nectarin I precursor. NEC1. germin-like protein.
BAA25197.1	AB012138	Lycopersicon esculentum	adaptation to Mn-deficiency. germin-like protein. Mdip1.
AAC78470.1	AF067731	Solanum tuberosum	germin-like protein. OXAOXA. similar to oxalate oxidase.
AAC25777.1	AF072694	Oryza sativa	germin-like protein 7. GER7. similar to wheat and barley oxalate oxidase.
AAC99473.1	AF039201	Pinus caribaea	germin-like protein. PcGER1.
CAA71051.1	Y09916	Triticum aestivum	germin homolog. pSBGer2.
AAC05146.1	AF049065	Pinus radiata	germin-like protein. PRGer1.
CAC34417.1	AJ311624	Pisum sativum	Germin-like protein. glp3.
SEQ ID NO: 915			
BAB19363.1	AP002542	Oryza sativa	putative beta-1,3-glucanase. P0679C08.2.
AAD10386.1	U72255	Oryza sativa	beta-1,3-glucanase precursor. Gns9.

CAB85903.1	AJ251646	<i>Pisum sativum</i>	hydrolysis of beta-1,3 conjugated glucans. beta-1,3 glucanase. gns2.
AAA90953.1	U30323	<i>Triticum aestivum</i>	beta 1,3-glucanase. Glc1.
BAA89481.1	AB029462	<i>Salix gilgiana</i>	beta-1,3-glucanase. SgGN1.
BAB40807.1	AB052291	<i>Pyrus pyrifolia</i>	catalyzing the hydrolysis of 1,3-beta-glucosyl linkages. endo-1,3-beta-glucanase-like protein. bgn-1. Amino acid alignment of the protein(BGN-1) encoded by pear pollen bgn-1 with barley endo-1,3-beta-glucanase(GII. accession number: pdb/1GHS-B/2.3/2/306/N/)(40% identity) and their hydrophobic cluster analysis(HCA)(a overall HCA homology score of 87.1%) showed that it was most likely that the bgn-1 encoded a endo-1,3-beta-glucanase. A higher identity(59.3%) was found between BGN-1 and a putative pea endo-1,3-beta-glucanase (accession number: dad/AJ251646-1).
AAB82772.2	AF001523	<i>Musa acuminata</i>	beta-1, 3-glucanase. similar to beta-1, 3-glucanase.
CAA49513.1	X69887	<i>Brassica napus</i>	beta-1,3-glucanase homologue.
AAF08679.1	AF004838	<i>Musa acuminata</i>	beta-1,3-glucanase.
CAA82271.1	Z28697	<i>Nicotiana tabacum</i>	beta-1,3-glucanase.
AAD10384.1	U72253	<i>Oryza sativa</i>	beta-1,3-glucanase precursor. Gns7.
CAB71021.1	AJ271598	<i>Hieracium piloselloides</i>	putative role in callose degradation. putative beta-1,3-glucanase. gluc.
CAA30261.1	X07280	<i>Nicotiana plumbaginifolia</i>	beta-glucanase.
AAA51643.1	M23120	<i>Nicotiana plumbaginifolia</i>	beta-glucanase precursor.
AAA87456.1	U22147	<i>Hevea brasiliensis</i>	beta-1,3-glucanase. HGN1. hydrolytic enzyme.
AAA34078.1	M63634	<i>Nicotiana plumbaginifolia</i>	regulator of beta(1,3)-glucanase. beta(1,3)-glucanase regulator.
AAD10385.1	U72254	<i>Oryza sativa</i>	beta-1,3-glucanase precursor. Gns8.
CAB38443.1	AJ133470	<i>Hevea brasiliensis</i>	beta-1,3-glucanase. hgn1.
AAB03501.1	U41323	<i>Glycine max</i>	beta-1,3-glucanase. SGN1.
AAA32939.1	M62907	<i>Hordeum vulgare</i>	hydrolysis of beta-(1-3)-glucan. (1-3)-beta-glucanase. cBGL32.

AAD33881.1	AF141654	Nicotiana tabacum	beta-1,3-glucanase. GGL4.
AAA03617.1	M80604	Lycopersicon esculentum	beta-1,3-glucanase.
BAA77786.1	AB027431	Oryza sativa	beta-1,3-glucanase.
BAA77787.1	AB027432	Oryza sativa	beta-1,3-glucanase.
CAB91554.1	AJ277900	Vitis vinifera	beta 1-3 glucanase. gl.
AAC14399.1	AF030771	Hordeum vulgare	beta-1,3-glucanase 2. BGL32.
CAA03908.1	AJ000081	Citrus sinensis	glucan hydrolase. beta-1,3-glucanase. gns1.
AAG24921.1	AF311749	Hevea brasiliensis	beta-1,3-glucanase.
AAA33946.1	M37753	Glycine max	beta-1,3-endoglucanase (EC 3.2.1.39).
AAA63542.1	M59443	Nicotiana tabacum	acidic beta-1,3-glucanase. glucanase.
AAD28732.1	AF112965	Triticum aestivum	beta-1,3-glucanase precursor. Glb3.
AAD10381.1	U72250	Oryza sativa	beta-1,3-glucanase precursor. Gns4.
CAA57255.1	X81560	Nicotiana tabacum	(1-)-beta-glucanase. Sp41a.
AAD33880.1	AF141653	Nicotiana tabacum	beta-1,3-glucanase. GGL1.
AAB86541.1	AF030166	Oryza sativa	glucanase. glul.
AAA63539.1	M60402	Nicotiana tabacum	glucan beta-1,3-glucanase. glucanase GLA.
AAA34053.1	M60464	Nicotiana tabacum	beta-1,3-glucanase.
AAD10380.1	U72249	Oryza sativa	beta-1,3-glucanase precursor. Gns3.
AAA63540.1	M60403	Nicotiana tabacum	glucan-1,3-beta-glucosidase. glucanase GLB.
SEQ ID NO: 916			
AAA85440.1	U32624	Sorghum bicolor	cytochrome P-450. CYP79. P450TYR; N-hydroxylase.

AAF27289.1	AF140613	Manihot esculenta	N-hydroxylating cytochrome P450. CYP79D1.
AAF27290.1	AF140614	Manihot esculenta	N-hydroxylating cytochrome P450. CYP79D2.
AAD03415.1	AF069494	Sinapis alba	converts tyrosine to para-hydroxyphenylacetaldoxime in para-hydroxybenzylglucosinolate biosynthesis. cytochrome P450. CYP79B1.
AAG59648.1	AC084319	Oryza sativa	putative cytochrome p450tyr. OSJNBa0004B24.15.
AAF66543.1	AF140609	Triglochin maritimum	cytochrome P450 CYP79E1. CYP79E1.
AAF66544.1	AF140610	Triglochin maritimum	cytochrome P450 CYP79E2. CYP79E2.
BAA92894.1	AB006790	Petunia x hybrida	cytochrome P450. IMT-2.
AAB94587.1	AF022458	Glycine max	CYP98A2p. CYP98A2. cytochrome P450 monooxygenase.
AAC32274.1	AF081575	Petunia x hybrida	flavonoid 3',5'-hydroxylase. Hfl. P450 enzyme.
AAD56282.1	AF155332	Petunia x hybrida	flavonoid 3'-hydroxylase. Htl. cytochrome P450; CYP75B2.
CAA64635.1	X95342	Nicotiana tabacum	cytochrome P450. hsr515. hypersensitivity-related gene.
CAA50155.1	X70824	Solanum melongena	flavonoid hydroxylase (P450). CYP75.
AAG44132.1	AF218296	Pisum sativum	cytochrome P450. P450 isolog.
AAA32913.1	M32885	Persea americana	cytochrome P-450LXXIA1 (cyp71A1).
BAA84071.1	AB028151	Antirrhinum majus	flavone synthase II. cytochrome P450. AFNS2.
AAD38930.1	AF135485	Glycine max	cytochrome P450 monooxygenase CYP93D1. CYP93E1.
AAB17562.1	U72654	Eustoma grandiflorum	flavonoid 3'5'-hydroxylase. F3'5'H. cytochrome P450; CYP75.
AAG34695.1	AF313492	Matthiola incana	putative cytochrome P450.
CAA65580.1	X96784	Nicotiana tabacum	cytochrome P450. hsr515.
BAA93634.1	AB025016	Lotus japonicus	cytochrome P450.
CAA71513.1	Y10489	Glycine max	putative cytochrome P450.

AAB94590.1	AF022461	Glycine max
CYP82C1p.	CYP82C1.	cytochrome P450 monooxygenase.
CAA71876.1	Y10982	Glycine max
		putative cytochrome P450.
BAA12159.1	D83968	Glycine max
		Cytochrome P-450 (CYP93A1).
AAG14962.1	AF214008	Brassica napus
		cytochrome p450-dependent monooxygenase. BNF5H2.
BAA74465.1	AB022732	Glycyrrhiza echinata
		cytochrome P450. CYP Ge-31.
BAA22422.1	AB001379	Glycyrrhiza echinata
		cytochrome P450. CYP81E1.
AAG14961.1	AF214007	Brassica napus
		cytochrome p450-dependent monooxygenase. BNF5H1.
CAA04117.1	AJ000478	Helianthus tuberosus
		fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1l. chimeric sequence (from 5'-race).
CAA04116.1	AJ000477	Helianthus tuberosus
		fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1c.
AAB94593.1	AF022464	Glycine max
CYP77A3p.	CYP77A3.	cytochrome P450 monooxygenase.
BAA13076.1	D86351	Glycine max
		cytochrome P-450 (CYP93A2).
CAA50647.1	X71656	Solanum melongena
		P450 hydroxylase.
SEQ ID NO: 918		
CAA06223.1	AJ004923	Lycopersicon esculentum
		Squalene epoxidase. ERG.
SEQ ID NO: 919		
AAF71823.1	AF153276	Populus tremula x Populus tremuloides
		pumilio domain-containing protein PPD1. PPD1. similar to Drosophila pumilio protein RNA-binding domain.
SEQ ID NO: 920		
BAA82393.1	AP000367	Oryza sativa
		EST C96716(C10608) corresponds to a region of the predicted gene.; Similar to putative receptor protein kinase. (AC002334).
CAC20842.1	AJ250467	Pinus sylvestris
		receptor protein kinase. upk.
AAB36558.1	U77888	Ipomoea nil
		receptor-like protein kinase INRPK1. inrpk1. leucine-rich repeat.
AAF91324.1	AF244890	Glycine max
		receptor-like protein kinase 3. RLK3. GmRLK3.

BAB40094.1	AP003210	Oryza sativa	putative receptor protein kinase. OSJNBa0010K01.7.
AAF91322.1	AF244888	Glycine max	receptor-like protein kinase 1. RLK1. GmRLK1.
AAC36318.1	AF053127	Malus x domestica	leucine-rich receptor-like protein kinase. LRPKml.
BAA84787.1	AP000559	Oryza sativa	ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).
BAA83373.1	AP000391	Oryza sativa	ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA (AC004484).
AAF59905.1	AF197946	Glycine max	receptor protein kinase-like protein. CLV1A.
AAK27806.1	AC022457	Oryza sativa	putative protein kinase. OSJNBa0006L06.21.
AAF91323.1	AF244889	Glycine max	receptor-like protein kinase 2. RLK2. GmRLK2.
AAF34426.1	AF172282	Oryza sativa	leucine rich repeat containing protein kinase. DUPR11.16.
AAK27817.1	AC022457	Oryza sativa	putative protein kinase. OSJNBa0006L06.16.
CAA61510.1	X89226	Oryza sativa	leucine-rich repeat/receptor protein kinase. lrk2.
BAB03621.1	AP002522	Oryza sativa	putative protein kinase Xa21. P0009G03.21.
AAB82755.1	U72725	Oryza longistaminata	receptor kinase-like protein. Xa21 gene family member A1; downstream of microsatellite region; disease resistance gene family member.
BAB03629.1	AP002522	Oryza sativa	putative protein kinase Xa21. P0009G03.30.
AAB61708.1	U93048	Daucus carota	somatic embryogenesis receptor-like kinase. SERK.
AAF66615.1	AF142596	Nicotiana tabacum	LRR receptor-like protein kinase.
AAB82756.1	U72724	Oryza sativa	receptor kinase-like protein. Xa21 gene family member E.
CAB51480.1	Y14600	Sorghum bicolor	putative protein serine /threonine kinase. RLK1. accumulates in mesophyll cells.
BAB39873.1	AP002882	Oryza sativa	putative protein kinase. P0439B06.8. contains ESTs AU056701(S20808),AU056702(S20808).

BAB18321.1	AP002865	Oryza sativa	putative receptor protein kinase. P0034C11.11.
BAB40081.1	AP003074	Oryza sativa	putative receptor protein kinase. OSJNBa0004G10.30.
AAD38286.1	AC007789	Oryza sativa	putative protein kinase. OSJNBa0049B20.13.
BAB21240.1	AP002953	Oryza sativa	Putative protein kinase. P0426D06.20. contains ESTs C22359(C11461),C22360(C11461).
AAK21965.1	AY028699	Brassica napus	receptor protein kinase PERK1.
BAA87853.1	AP000816	Oryza sativa	EST AU030604(E51294) corresponds to a region of the predicted gene. Similar to putative NAK-like Ser/Thr protein kinase. (AF001308).
BAB16871.1	AP002537	Oryza sativa	putative protein kinase APK1A.Arabidopsis thaliana. P0001B06.24. contains ESTs C22608(R3192),D25110(R3192).
AAC27894.1	AF023164	Zea mays	leucine-rich repeat transmembrane protein kinase 1. ltk1.
AAK00425.1	AC069324	Oryza sativa	Putative protein kinase. OSJNBa0071K19.11.
AAG59657.1	AC084319	Oryza sativa	putative protein kinase. OSJNBa0004B24.20.
BAA94519.1	AP001800	Oryza sativa	ESTs AU032341(R3918),AU071016(R10613) correspond to a region of the predicted gene. Similar to Arabidopsis thaliana chromosome 4, BAC F9D16; putative receptor kinase (AL035394).
BAB07903.1	AP002835	Oryza sativa	putative receptor kinase. P0417G05.10. contains ESTs AU032341(R3918),AU071016(R10613).
SEQ ID NO: 921			
BAA96250.1	AB027617	Pyrus pyrifolia	UDP-glucose pyrophosphorylase.
BAA25917.1	AB013353	Pyrus pyrifolia	UDP-glucose pyrophosphorylase.
CAA62689.1	X91347	Hordeum vulgare	UDP-glucose pyrophosphorylase.
AAF62555.1	AF249880	Oryza sativa subsp. indica	UDP-glucose pyrophosphorylase. UDPGase.
SEQ ID NO: 922			
AAD03415.1	AF069494	Sinapis alba	converts tyrosine to para-hydroxyphenylacetaldoxime in para-hydroxybenzylglucosinolate biosynthesis. cytochrome P450. CYP79B1.

AAA85440.1	U32624	<i>Sorghum bicolor</i> cytochrome P-450. CYP79. P450TYR; N-hydroxylase.
AAF27289.1	AF140613	<i>Manihot esculenta</i> N-hydroxylating cytochrome P450. CYP79D1.
AAF27290.1	AF140614	<i>Manihot esculenta</i> N-hydroxylating cytochrome P450. CYP79D2.
AAG59648.1	AC084319	<i>Oryza sativa</i> putative cytochrome p450tyr. OSJNBa0004B24.15.
AAF66543.1	AF140609	<i>Triglochin maritimum</i> cytochrome P450 CYP79E1. CYP79E1.
AAF66544.1	AF140610	<i>Triglochin maritimum</i> cytochrome P450 CYP79E2. CYP79E2.
BAA92894.1	AB006790	<i>Petunia x hybrida</i> cytochrome P450. IMT-2.
AAD56282.1	AF155332	<i>Petunia x hybrida</i> flavonoid 3'-hydroxylase. Ht1. cytochrome P450; CYP75B2.
CAA50155.1	X70824	<i>Solanum melongena</i> flavonoid hydroxylase (P450). CYP75.
AAC32274.1	AF081575	<i>Petunia x hybrida</i> flavonoid 3',5'-hydroxylase. Hf1. P450 enzyme.
AAG34695.1	AF313492	<i>Matthiola incana</i> putative cytochrome P450.
AAA32913.1	M32885	<i>Persea americana</i> cytochrome P-450LXXIA1 (cyp71A1).
CAA64635.1	X95342	<i>Nicotiana tabacum</i> cytochrome P450. hsr515. hypersensitivity-related gene.
CAA65580.1	X96784	<i>Nicotiana tabacum</i> cytochrome P450. hsr515.
AAB94587.1	AF022458	<i>Glycine max</i> CYP98A2p. CYP98A2. cytochrome P450 monooxygenase.
AAB17562.1	U72654	<i>Eustoma grandiflorum</i> flavonoid 3'5'-hydroxylase. F3'5'H. cytochrome P450; CYP75.
AAG09208.1	AF175278	<i>Pisum sativum</i> wound-inducible P450 hydroxylase. CYP82A1.
AAD37433.1	AF150881	<i>Lycopersicon esculentum x Lycopersicon peruvianum</i> catalyzes the hydroxylation of ferulic acid to 5-hydroxyferulic acid. ferulate-5-hydroxylase. CYP84. cytochrome P450-dependent monooxygenase; F5H; FAH1.
CAA04117.1	AJ000478	<i>Helianthus tuberosus</i> fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1l. chimeric sequence (from 5'- race).
CAA04116.1	AJ000477	<i>Helianthus tuberosus</i> fatty acid in-chain hydroxylase. cytochrome P450. CYP81B1c.

CAB43505.1	AJ239051	Cicer arietinum	cytochrome P450. cyp81E2.
AAC49188.2	U29333	Pisum sativum	cytochrome P450 monooxygenase. CYP82. new cytochrome P450 family.
AAG14963.1	AF214009	Brassica napus	cytochrome p450-dependent monooxygenase. BNF5H3.
AAD38930.1	AF135485	Glycine max	cytochrome P450 monooxygenase CYP93D1. CYP93E1.
AAG14962.1	AF214008	Brassica napus	cytochrome p450-dependent monooxygenase. BNF5H2.
AAG44132.1	AF218296	Pisum sativum	cytochrome P450. P450 isolog.
AAB94588.1	AF022459	Glycine max	CYP71D10p. CYP71D10. cytochrome P450 monooxygenase.
AAG14961.1	AF214007	Brassica napus	cytochrome p450-dependent monooxygenase. BNF5H1.
AAB94590.1	AF022461	Glycine max	CYP82C1p. CYP82C1. cytochrome P450 monooxygenase.
CAA71513.1	Y10489	Glycine max	putative cytochrome P450.
BAA84071.1	AB028151	Antirrhinum majus	flavone synthase II. cytochrome P450. AFNS2.
CAA50442.1	X71130	Petunia x hybrida	P450 hydroxylase. PET 1.

SEQ ID NO: 924

BAB20581.1	AB042268	Zea mays	response regulator 6. ZmRR6.
AAK14395.1	AF339732	Dianthus caryophyllus	response regulator protein. RR.
BAB20580.1	AB042267	Zea mays	response regulator 5. ZmRR5.
BAB20579.1	AB042261	Zea mays	response regulator 4. ZmRR4.
BAA85113.1	AB031012	Zea mays	response regulator 2. ZmRR2. cytokinin-inducible.
BAA82873.1	AB024291	Zea mays	response regulator. ZmRR2.
BAA75253.1	AB004882	Zea mays	response regulator. ZmCip1, cytokinin-inducible protein.
BAA85112.1	AB031011	Zea mays	response regulator 1. ZmRR1. cytokinin-inducible.

BAB17300.1 AB042260 Zea mays
response regulator. ZmRR3.

BAB20582.1 AB042269 Zea mays
response regulator 7. ZmRR7.

BAB41137.1 AB060130 Zea mays
response regulator 8. ZmRR8.

SEQ ID NO: 925

AAA33280.1 L20475 Datura stramonium
29kDa protein; high homology to aa sequence of tropinone reductases.

AAA33281.1 L20473 Datura stramonium
catalyses a stereospecific reduction of tropinone to tropine. tropinone reductase-I.

BAA85844.1 AB026544 Hyoscyamus niger
tropinone reductase-I. tr1.

CAC34420.1 AJ307584 Solanum tuberosum
tropine forming tropinone reductase. tropinone reductase I. TRI.

BAA13547.1 D88156 Hyoscyamus niger
tropinone reductase-I.

AAA33282.1 L20474 Datura stramonium
catalyses a stereospecific reduction of tropinone to pseudotropine. tropinone reductase-II.

BAA85845.1 AB026545 Hyoscyamus niger
tropinone reductase-II. tr2.

AAB09776.1 L20485 Hyoscyamus niger
tropinone reductase-II.

CAB52307.1 AJ245634 Solanum tuberosum
pseudotropine forming tropinone reductase. tropinone reductase II. TRII.

CAC19810.1 AJ292343 Solanum tuberosum
pseudotropine forming tropinone reductase. tropinone reductase II. trII.

CAA45866.1 X64566 Cuphea lanceolata
beta-ketoacyl-ACP reductase. Clkr27. 3-oxoacyl-[acyl-carrier protein] reductase.

CAA45793.1 X64463 Brassica napus
3-oxoacyl-[acyl-carrier protein] reductase.

AAB82767.1 U89509 Zea mays
cuticular wax biosynthesis. b-keto acyl reductase. glossy8.

AAB82766.1 U89510 Hordeum vulgare
cuticular wax biosynthesis. b-keto acyl reductase. glossy8.

AAB20114.2 S60064 Brassica napus
enoyl-acyl carrier protein reductase. This sequence comes from fig3; conceptual translation differs from published sequence.

CAA74176.1 Y13861 Nicotiana tabacum
enoyl-ACP reductase. enr-T2.

AAB82764.1 U89511 Allium porrum
cuticular wax biosynthesis. b-keto acyl reductase. glossy8.

AAC78100.1	AF093628	Oryza sativa	protochlorophyllide reductase homolog.
CAA74177.1	Y13862	Nicotiana tabacum	enoyl-ACP reductase. enr-T1.
SEQ ID NO: 927			
AAD43046.1	AF124045	Sorghum bicolor	GTP-binding protein-like. 110K5.8. terminal exon, defined by homology to maize ESTs.
SEQ ID NO: 928			
CAA09619.1	AJ011418	Lycopersicon esculentum	ubiquitin activating enzyme.
AAC32140.1	AF051239	Picea mariana	probable ubiquitin activating enzyme 2. Sb53. similar to Arabidopsis thaliana ubiquitin activating enzyme 2 encoded by GenBank Accession Number U40566.
AAA34308.1	M55604	Triticum aestivum	ubiquitin-activating enzyme E1. UBA1.
AAA34265.1	M90663	Triticum aestivum	ubiquitin activating enzyme. E1.
AAA34266.1	M90664	Triticum aestivum	ubiquitin activating enzyme. E1.
CAA71762.1	Y10804	Nicotiana tabacum	Ubiquitin activating enzyme E1. UBA1.
SEQ ID NO: 929			
CAA55693.1	X79086	Zea mays	initiator-binding protein. IBP2.
CAC19789.1	AJ251686	Catharanthus roseus	putative transcription factor. MYB-like DNA-binding protein. bpf-1.
CAA55691.1	X79085	Zea mays	initiator binding protein. IBP1.
AAF97508.1	AF242298	Oryza sativa	telomere binding protein-1. TBP1.
SEQ ID NO: 930			
AAK15447.1	AC037426	Oryza sativa	putative flavin-containing monooxygenase. OSJNBb0014I11.12.
AAK15439.1	AC037426	Oryza sativa	putative flavin-containing monooxygenase. OSJNBb0014I11.8.
BAA88198.1	AP000837	Oryza sativa	Similar to human dimethylaniline monooxygenase (AC002376).
BAA88195.1	AP000837	Oryza sativa	Similar to human dimethylaniline monooxygenase (AC002376).
BAB32703.1	AP002902	Oryza sativa	dimethylaniline monooxygenase-like protein. P0492F05.5. contains EST C72123(E1029).

BAB07916.2 AP002835 *Oryza sativa*
dimethylaniline monooxygenase-like protein. P0417G05.24. contains EST C72123(E1029).

SEQ ID NO: 931

AAG38521.1 AF283536 *Citrus x paradisi*
cystatin-like protein. cystein proteinase inhibitor.

AAA97905.1 U51853 *Glycine max*
cysteine proteinase inhibitor.

CAA79954.1 Z21954 *Vigna unguiculata*
cysteine proteinase inhibitor.

AAB66355.1 U54702 *Oryza sativa*
thiol proteinase inhibitor; cysteine proteinase inhibitor. oryzacystatin. has potential for insect resistance in rice and for cancer therapeutics.

AAB24010.1 S49967 *Oryza*
oryzacystatin. oryzacystatin. cysteine protease inhibitor; This sequence comes from Fig. 1.

CAA60610.1 X87126 *Zea mays*
cysteine proteinase inhibitor. zmc-II.

BAA09666.1 D63342 *Zea mays*
cysteine proteinase inhibitor. gCC.

AAA32672.1 L16624 *Ambrosia artemisiifolia*
cystatin proteinase inhibitor.

BAA07327.1 D38130 *Zea mays*
inhibition against cysteine proteinases. cystatin II.

AAA97907.1 U51855 *Glycine max*
cysteine proteinase inhibitor.

BAB18766.1 AB038392 *Triticum aestivum*
cysteine proteinase inhibitor. WC61. cystatin.

BAB18767.1 AB038393 *Triticum aestivum*
cysteine proteinase inhibitor. WC92. cystatin.

CAA11899.1 AJ224331 *Castanea sativa*
cysteine proteinase inhibitor. cystatin.

AAB71505.1 U82220 *Pyrus communis*
cysteine protease inhibitor.

AAA79239.1 L48182 *Brassica rapa*
cysteine proteinase inhibitor. N-terminal deletion clone; putative.

CAA60634.1 X87168 *Sorghum bicolor*
cysteine proteinase inhibitor. CPI1.

AAA68150.1 L42819 *Brassica rapa*
cysteine protenase inhibitor. N-terminal deletion clone; putative.

BAB18765.1 AB038391 *Triticum aestivum*
cysteine proteinase inhibitor. gWC2. cystatin.

BAB18768.1 AB038394 *Triticum aestivum*
cysteine proteinase inhibitor. WC83. cystatin.

AAC37479.1	L41355	Brassica rapa	cysteine proteinase inhibitor.
BAA28867.1	AB014760	Cucumis sativus	root-specific cystein protease inhibitor. cystein proteinase inhibitor.
AAD33907.1	AF143677	Artemisia vulgaris	cysteine proteinase inhibitor. CPI. pollen cystatin.
BAA89582.1	AP001073	Oryza sativa	ESTs AU067919(C10906),AU067918(C10906) correspond to a region of the predicted gene. Similar to cysteine proteinase inhibitor (D31700).
CAA72790.1	Y12068	Hordeum vulgare	cysteine proteinase inhibitor. CPI.
AAA96316.1	U51119	Brassica rapa	cysteine proteinase inhibitor. BCPI-2.
AAK15090.1	AF240007	Sesamum indicum	cystatin. cysteine proteinase inhibitor.
AAF23127.1	AF198389	Lycopersicon esculentum	cysteine proteinase inhibitor. cystatin. STC. expression induced by arachidonic acid and gamma linolenic acid.
BAA19610.1	D64115	Glycine max	cysteine proteinase inhibitor. cystatin.
BAA19608.1	D31700	Glycine max	cysteine proteinase inhibitor. cystatin.
CAA89697.1	Z49697	Ricinus communis	cysteine proteinase inhibitor.
AAF72202.1	AF265551	Manihot esculenta	cysteine protease inhibitor.
AAA97906.1	U51854	Glycine max	cysteine proteinase inhibitor.
CAA50437.1	X71124	Carica papaya	cysteine proteinase inhibitor (cystatin).
AAF23126.1	AF198388	Lycopersicon esculentum	cysteine proteinase inhibitor. cystatin. LTC. expression induced by arachidonic acid and gamma linolenic acid.
AAD13812.1	AF117334	Ipomoea batatas	cysteine proteinase inhibitor. cystatin.
AAF64480.1	AF241536	Ipomoea batatas	cysteine protease inhibitor. CYSPI.
AAK30004.1	AY028994	Dianthus caryophyllus	cysteine proteinase inhibitor. DC-CPI _n .
BAB18769.1	AB038395	Triticum aestivum	cysteine proteinase inhibitor. WC81. cystatin.
AAC32853.1	AF083253	Lycopersicon esculentum	cysteine protease inhibitor.

SEQ ID NO: 938

CAA06486.1 AJ005340 *Linum usitatissimum*
IAA amidohydrolase. homolog.

SEQ ID NO: 940

BAB17350.1 AP002747 *Oryza sativa*
putative nodulin. P0698G03.34. contains ESTs
D39891(S1543),D41717(S4395),AU033037(S1543).

BAA85440.1 AP000616 *Oryza sativa*
ESTs AU055729(S20023),AU055730(S20023) correspond to a region of the predicted gene.;
similar to Medicago nodulin N21-like protein (AC004218).

CAB53493.1 AJ245900 *Oryza sativa*
CAA303720.1 protein. q3037.20. Similar to Medicago nodulin N21 (MtN21).

SEQ ID NO: 941

BAA21921.1 AB006599 *Petunia x hybrida*
ZPT2-12. C2H2 zinc finger protein, 2 finger.

BAA21922.1 AB006600 *Petunia x hybrida*
ZPT2-13. C2H2 zinc finger protein, 2finger.

BAA19110.1 AB000451 *Petunia x hybrida*
PETHy;ZPT2-5. Cys(2) His(2) zinc finger protein, 2 fingers.

BAA21923.1 AB006601 *Petunia x hybrida*
ZPT2-14. C2H2 zinc finger protein, 2 finger.

BAA21925.1 AB006603 *Petunia x hybrida*
ZPT2-8. C2H2 zinc finger protein, 2 finger.

BAA21924.1 AB006602 *Petunia x hybrida*
ZPT2-7. C2H2 zinc finger protein, 2finger.

BAA21920.1 AB006598 *Petunia x hybrida*
ZPT2-11. C2H2 zinc finger protein, 2finger.

CAA60828.1 X87374 *Pisum sativum*
putative zinc finger protein.

BAA19111.1 AB000452 *Petunia x hybrida*
PETHy;ZPT2-6. Cys(2) His(2) zinc finger protein, 2 fingers.

BAA21926.1 AB006604 *Petunia x hybrida*
ZPT2-9. C2H2 zinc finger protein, 2 finger.

BAA21927.1 AB006605 *Petunia x hybrida*
ZPT3-3. C2H2 zinc finger protein, 3 finger.

BAA96071.1 AB035133 *Petunia x hybrida*
C2H2 zinc-finger protein ZPT3-3. ZPT3-3.

BAA21919.1 AB006597 *Petunia x hybrida*
ZPT2-10. C2H2 zinc finger protein, 2 finger.

BAA96070.1 AB035132 *Petunia x hybrida*
C2H2 zinc-finger protein ZPT2-10. PETHy;ZPT2-10.

CAB77055.1 Y18788 *Medicago sativa*
putative TFIIIA (or kruppel)-like zinc finger protein.

AAB53260.1 U76554 Brassica rapa
transcription factor. zinc-finger protein-1. BR42.

AAB53261.1 U76555 Brassica rapa
zinc-finger protein BcZFP1. BcZFP1(3-2z).

BAA19114.1 AB000455 Petunia x hybrida
PETHy;ZPT4-1. Cys(2) His(2) zinc finger protein, 4 fingers.

BAA05078.1 D26085 Petunia x hybrida
zinc-finger DNA binding protein.

AAD26942.1 AF119050 Datisca glomerata
zinc-finger protein 1. zfp1. DgZFP1.

BAA05077.1 D26084 Petunia x hybrida
zinc-finger DNA binding protein.

AAB39638.1 U68763 Glycine max
putative transcription factor. SCOF-1. scof-1. zinc-finger protein.

AAC06243.1 AF053077 Nicotiana tabacum
transcription factor. osmotic stress-induced zinc-finger protein. zfp.

BAA19112.1 AB000453 Petunia x hybrida
PETHy;ZPT3-1. Cys(2) His(2) zinc finger protein, 3 fingers.

AAK01713.1 AF332876 Oryza sativa
zinc finger transcription factor ZF1.

BAA05076.1 D26083 Petunia x hybrida
zinc-finger DNA binding protein.

BAA05079.1 D26086 Petunia x hybrida
zinc-finger protein.

BAA21928.1 AB006606 Petunia x hybrida
ZPT4-4. C2H2 zinc finger protein, 4 finger.

BAA19926.1 AB000456 Petunia x hybrida
PETHy; ZPT4-2. C2H2 zinc finger protein, 4 finger.

BAA19113.1 AB000454 Petunia x hybrida
PETHy;ZPT3-2. Cys(2) His(2) zinc finger protein, 3 fingers.

SEQ ID NO: 945

AAG10793.1 AF296158 Citrus unshiu
beta-carotene hydroxylase. CHX1.

AAG33636.1 AF315289 Citrus unshiu
beta-carotene hydroxylase. CHX2. similar to beta-carotene hydroxylase of Citrus unshiu
encoded by GenBank Accession Number AF296158.

AAG10430.1 AF251018 Tagetes erecta
beta hydroxylase.

CAB55625.1 Y14809 Lycopersicon esculentum
beta-carotene hydroxylase. CrtR-b1.

CAA70888.1 Y09722 Capsicum annuum
beta-carotene hydroxylase 2.

CAB55626.1 Y14810 *Lycopersicon esculentum*
beta-carotene hydroxylase. CrtR-b2.

CAA70427.1 Y09225 *Capsicum annuum*
beta-carotene hydrolase.

CAC06712.1 AJ278882 *Narcissus pseudonarcissus*
synthesis of zeaxanthin. beta-carotene hydroxylase.

AAD54243.1 AF162276 *Haematococcus pluvialis*
carotenoid hydroxylase.

SEQ ID NO: 946

AAC18914.1 U94748 *Petunia x hybrida*
AN11. An11. No functional information available. Protein is involved in transcriptional regulation of anthocyanin biosynthesis in petunia. Protein contains five WD 40 repeats; WD 40 repeat protein.

SEQ ID NO: 948

AAG52887.1 AF333386 *Nicotiana tabacum*
beta-expansin-like protein. PPAL. pollen allergen-like protein.

AAF72986.1 AF261273 *Oryza sativa*
putative cell wall loosening activity. beta-expansin. EXPB5.

AAF72990.1 AF261277 *Oryza sativa*
putative cell wall loosening activity. beta-expansin. EXPB9. putative group-1 pollen allergen.

BAB20817.1 AB051899 *Atriplex lentiformis*
beta-expansin. Al-EXP1.

AAF72984.1 AF261271 *Oryza sativa*
putative cell wall loosening activity. beta-expansin. EXPB3.

AAK15453.1 AC037426 *Oryza sativa*
beta-expansin EXPB3. OSJNBb0014I11.1.

AAF72991.1 AF261278 *Oryza sativa*
putative cell wall loosening activity. beta-expansin. EXPB10. putative group-1 pollen allergen.

AAK15442.1 AC037426 *Oryza sativa*
beta-expansin EXPB6. OSJNBb0014I11.3.

AAF72987.1 AF261274 *Oryza sativa*
putative cell wall loosening activity. beta-expansin. EXPB6.

AAF72983.1 AF261270 *Oryza sativa*
putative cell wall loosening activity. beta-expansin. EXPB1. putative group-1 pollen allergen
Ory s1.

AAF72988.1 AF261275 *Oryza sativa*
putative cell wall loosening activity. beta-expansin. EXPB7.

AAF72989.2 AF261276 *Oryza sativa*
putative cell wall loosening activity. beta-expansin. EXPB8.

AAF72985.1 AF261272 *Oryza sativa*
putative cell wall loosening activity. beta-expansin. EXPB4.

AAK15440.1	AC037426	Oryza sativa	beta-expansin EXPB2. OSJNBb0014I11.2.
AAB61710.1	U95968	Oryza sativa	beta-expansin. EXPB2. cell wall loosening protein.
AAB37749.1	U30460	Cucumis sativus	expansin S2 precursor. Cs-EXP2. similar to pollen allergen Lol pI, Lolium perenne, Swiss-Prot Accession Number P14946; former gene name CuExS2; expansin-30 (Ex30) protein.
AAD38296.1	AC007789	Oryza sativa	putative expansin. OSJNBa0049B20.23.
BAB18336.1	AP002865	Oryza sativa	putative expansin. P0034C11.27.
CAC19183.1	AJ291816	Cicer arietinum	expansin.
AAG13983.1	AF297522	Prunus avium	expansin 2. Exp2. PruavExp2.
AAG01875.1	AF291659	Striga asiatica	alpha-expansin 3. Exp3.
AAG32920.1	AF184232	Lycopersicon esculentum	expansin. Exp8.
AAC96077.1	AF049350	Nicotiana tabacum	involved in acid-growth response. alpha-expansin precursor. Nt-EXP1. cell wall protein.
AAC96078.1	AF049351	Nicotiana tabacum	involved in acid-growth response. alpha-expansin precursor. Nt-EXP2. cell wall protein.
AAF35902.1	AF230333	Zinnia elegans	expansin 3.
BAA88200.1	AP000837	Oryza sativa	EST AU078708(E60526) corresponds to a region of the predicted gene. Similar to expansin (U85246).
AAC39512.1	AF043284	Gossypium hirsutum	expansin. GhEX1. contains N-terminal signal peptide.
AAD38297.1	AC007789	Oryza sativa	putative expansin. OSJNBa0049B20.24.
AAF32411.1	AF230278	Triphysaria versicolor	alpha-expansin 1.
BAB18338.1	AP002865	Oryza sativa	putative expansin. P0034C11.29.
AAG32921.1	AF184233	Lycopersicon esculentum	expansin. Exp10.
CAC19184.1	AJ291817	Cicer arietinum	expansin.
AAC96079.1	AF049352	Nicotiana tabacum	involved in acid-growth response. alpha-expansin precursor. Nt-EXP3. cell wall protein.

SEQ ID NO: 950

CAA52213.1	X74115	<i>Picea abies</i>	short-chain alcohol dehydrogenase.
AAC35342.1	AF072449	<i>Ipomoea trifida</i>	short-chain alcohol dehydrogenase. SSP. self-incompatibility-locus specific stigma protein.
AAC35340.1	AF072447	<i>Ipomoea trifida</i>	short-chain alcohol dehydrogenase. SSP. self-incompatibility-locus specific stigma protein.
CAA11153.1	AJ223177	<i>Nicotiana tabacum</i>	short chain alcohol dehydrogenase.
CAA11154.1	AJ223178	<i>Nicotiana tabacum</i>	short chain alcohol dehydrogenase. SCANT.
AAK29646.1	AF349916	<i>Solanum tuberosum</i>	putative short-chain type alcohol dehydrogenase. GAN; similar to tomato Leert10 and maize Ts2.
AAC37345.1	L20621	<i>Zea mays</i>	alcohol dehydrogenase. short chain.
AAC35341.1	AF072448	<i>Ipomoea trifida</i>	short-chain alcohol dehydrogenase. SSP. self-incompatibility-locus specific stigma protein.
AAC35343.1	AF072450	<i>Ipomoea trifida</i>	short-chain alcohol dehydrogenase. SSP. self-incompatibility-locus specific stigma protein.
AAB57737.1	U89270	<i>Tripsacum dactyloides</i>	short-chain alcohol dehydrogenase. gynomonoeious sex form 1. similar to <i>Zea mays</i> tasselseed 2: SwissProt Accession Number P50160.
AAF89645.1	AF169018	<i>Glycine max</i>	seed maturation protein PM34. PM34. similar to bacterial glucose and ribitol dehydrogenase.
AAF04253.1	AF097651	<i>Pisum sativum</i>	short-chain alcohol dehydrogenase SAD-C. sadC. contains the entire nucleotide binding motif of 3(alpha), 20(beta)-hydroxysteroid dehydrogenases, GXXXXXXGXXG(A)XGXXXXA (Ghosh et al., 1991, Proc. Natl. Acad. Sci. USA 88, 10064-10068).
AAF04193.1	AF053638	<i>Pisum sativum</i>	short-chain alcohol dehydrogenase. sadA. contains the entire nucleotide binding motif of the 3(alfa),20(beta)-hydroxysteroid dehydrogenase: GXXXXXXGXXG(A)XGXXXXA (Ghosh et al. (1991) Proc. Natl. Acad. Sci. USA 88, 10064-10068); similar to <i>Lycopersicon esculentum</i> product encoded by GenBank Accession Number U21801 and <i>Streptomyces hydrogenans</i> steroid alcohol dehydrogenase.
AAB57738.1	U89271	<i>Tripsacum dactyloides</i>	short-chain alcohol dehydrogenase. gynomonoeious sex form 1. similar to <i>Zea mays</i> tasselseed 2: SwissProt Accession Number P50160.
CAB91875.1	AJ277945	<i>Lycopersicon esculentum</i>	putative alcohol dehydrogenase. yfe37.
AAF04194.1	AF053639	<i>Pisum sativum</i>	short-chain alcohol dehydrogenase. sadB. contains the Prosite pattern no. PS00061 for short-chain alcohol dehydrogenases; contains a deletion in the nucleotide binding motif of the 3(alfa),20(beta)-hydroxysteroid dehydrogenase: GXXXXXXGXXG(A)XGXXXXA (Ghosh et al. (1991) Proc. Natl. Acad. Sci. USA 88, 10064-10068).

AAB00109.1	U21801	Lycopersicon esculentum	alcohol dehydrogenase homolog. GAD3. mRNA is suppressed in the presence of gibberellin; similar to nonmetallo-short-chain alcohol dehydrogenases, PIR Accession Number A47542.
SEQ ID NO: 952			
CAB63264.1	AJ251808	Lotus japonicus	calcium-binding protein. cbp1.
AAG43547.1	AF211529	Nicotiana tabacum	Avr9/Cf-9 rapidly elicited protein 31. ACRE31. similar to Solanum tuberosum CAST calcium binding protein encoded by GenBank Accession Number L02830.
AAA34014.1	L01432	Glycine max	calcium-binding regulatory protein. calmodulin. SCaM-3. putative.
AAA34013.1	L01430	Glycine max	calcium-binding regulatory protein. calmodulin. SCaM-1. putative.
AAA92681.1	U13882	Pisum sativum	calcium-binding protein. calmodulin.
CAA78301.1	Z12839	Lilium longiflorum	calcium binding protein, signal transduction. calmodulin.
AAA33397.1	L18912	Lilium longiflorum	calcium binding protein, signal transduction. calmodulin. putative.
AAA19571.1	U10150	Brassica napus	calcium binding. calmodulin. bcml.
AAA85157.1	U20297	Solanum tuberosum	calcium-binding protein. calmodulin.
AAA85156.1	U20296	Solanum tuberosum	calcium-binding protein. calmodulin.
AAA62351.1	U20295	Solanum tuberosum	calcium-binding protein. calmodulin.
AAA85155.1	U20294	Solanum tuberosum	calcium-binding protein. calmodulin.
AAC49587.1	U49105	Triticum aestivum	calmodulin TaCaM4-1. calcium-binding protein.
AAC49586.1	U49104	Triticum aestivum	calmodulin TaCaM3-3. calcium-binding protein.
AAC49585.1	U49103	Triticum aestivum	calmodulin TaCaM3-2. calcium-binding protein.
AAC49584.1	U48693	Triticum aestivum	calmodulin TaCaM3-1. calcium-binding protein.
AAC49580.1	U48689	Triticum aestivum	calmodulin TaCaM1-3. calcium-binding protein.
AAC49579.1	U48688	Triticum aestivum	calmodulin TaCaM1-2. calcium binding protein.
AAC49578.1	U48242	Triticum aestivum	calmodulin TaCaM1-1. calcium-binding.

CAA78287.1 Z12827 Oryza sativa
calcium binding protein, signal transduction. calmodulin.

AAA03580.1 L01431 Glycine max
calcium-binding regulatory protein. calmodulin. SCaM-2. putative.

AAA33901.1 L18913 Oryza sativa
calcium binding protein, signal transduction. calmodulin. putative.

AAA34015.1 L01433 Glycine max
calcium-binding regulatory protein. calmodulin. SCaM-4. putative.

Table 24 Plant Open Reading Frames (ORFs) orthologous to specific *Chenopodium* ORFs

SEQ ID NO:1956	
CAB51903.1	AJ242807 <i>Brassica napus</i> endo-1,4-beta-D-glucanase. Cel16. cellulase.
BAA94257.1	AB040769 <i>Hordeum vulgare</i> endo-1,4-beta-glucanase Cel1. Cell.
AAC49704.1	U78526 <i>Lycopersicon esculentum</i> endo-1,4-beta-glucanase. Cel3.
SEQ ID NO:1957	
BAB21273.1	AP002844 <i>Oryza sativa</i> putative ABC transporter protein. P0410E03.4.
BAB21275.1	AP002844 <i>Oryza sativa</i> putative ABC transporter protein. P0410E03.6.
BAB21276.1	AP002844 <i>Oryza sativa</i> putative ABC transporter protein. P0410E03.7. contains EST D22472(C1173).
CAA94437.1	Z70524 <i>Spirodela polyrrhiza</i> multidrug resistance protein. PDR5-like ABC transporter.
BAB21279.1	AP002844 <i>Oryza sativa</i> putative ABC transporter protein. P0410E03.10. contains ESTs AU065360(R3463),AU101680(R3463).
CAA03960.1	AJ000234 <i>Hordeum vulgare</i> partial sequence, homology to PDR5-like ABC transporter.
SEQ ID NO:1960	
AAD51778.1	AF116858 <i>Phaseolus vulgaris</i> utilizes UDPX as the sugar donor and catalyzes the formation of O-xylosylzeatin from zeatin. zeatin O-xylosyltransferase. ZOX1.
AAD04166.1	AF101972 <i>Phaseolus lunatus</i> catalyzes formation of O-glucosylzeatin from zeatin and UDPG; catalyzes formation of O-xylosylzeatin from zeatin and UDPX. zeatin O-glucosyltransferase. ZOG1. cytokinin O-glucosyltransferase.
BAA36410.1	AB012114 <i>Vigna mungo</i> UDP-glycose:flavonoid glycosyltransferase. UFGlyT.
BAB17061.1	AP002523 <i>Oryza sativa</i> putative glucosyl transferase. P0013F10.7. contains EST C73149(E2992).

BAA36412.1 AB012116 *Vigna mungo*
 UDP-glycose:flavonoid glycosyltransferase. UFGlyT.

AAK28303.1 AF346431 *Nicotiana tabacum*
 phenylpropanoid:glucosyltransferase 1. togt1.
 glucosyltransferase.

BAB17059.1 AP002523 *Oryza sativa*
 putative glucosyl transferase. P0013F10.5.

AAF17551.1 AF198453 *Glycine max*
 UDP-glycose:flavonoid glycosyltransferase. UFGlyT.

AAB36653.1 U32644 *Nicotiana tabacum*
 immediate-early salicylate-induced glucosyltransferase.
 IS5a.

CAB88666.1 AJ400861 *Cicer arietinum*
 flavonoid glycosyltransferase. putative UDP-glycose.

AAB36652.1 U32643 *Nicotiana tabacum*
 immediate-early salicylate-induced glucosyltransferase.
 IS10a.

CAA54612.1 X77462 *Manihot esculenta*
 UTP-glucose glucosyltransferase. CGT5.

BAB17060.1 AP002523 *Oryza sativa*
 putative glucosyl transferase. P0013F10.6.

AAK28304.1 AF346432 *Nicotiana tabacum*
 phenylpropanoid:glucosyltransferase 2. togt2.
 glucosyltransferase.

CAA59450.1 X85138 *Lycopersicon esculentum*
 twil. homologous to glucosyltransferases.

BAA83484.1 AB031274 *Scutellaria baicalensis*
 UDP-glucose: flavonoid 7-O-glucosyltransferase. ufgt.

CAA54611.1 X77461 *Manihot esculenta*
 UTP-glucose glucosyltransferase. CGT2.

BAA36411.1 AB012115 *Vigna mungo*
 UDP-glycose:flavonoid glycosyltransferase. UFGlyT.

CAC35167.1 AJ310148 *Rauvolfia serpentina*
 arbutin synthase. as.

BAB17182.1 AP002843 *Oryza sativa*
 putative UTP-glucose glucosyltransferase. P0407B12.19.

CAB56231.1 Y18871 *Dorotheanthus bellidiformis*
betanidin-5-O-glucosyltransferase.

BAB17176.1 AP002843 *Oryza sativa*
putative UTP-glucose glucosyltransferase. P0407B12.13.

AAK16172.1 AC079887 *Oryza sativa*
putative glucosyltransferase. OSJNBa0040E01.14.

CAA54613.1 X77463 *Manihot esculenta*
UTP-glucose glucosyltransferase. CGT6.

AAF61647.1 AF190634 *Nicotiana tabacum*
UDP-glucose:salicylic acid glucosyltransferase. SA-GTase.

BAA93039.1 AB033758 *Citrus unshiu*
limonoid UDP-glucosyltransferase. LGTase.

CAA54610.1 X77460 *Manihot esculenta*
UTP-glucose glucosyltransferase. CGT4.

AAA59054.1 L34847 *Zea mays*
conjugation of the growth hormone indole-3-acetic acid
(IAA). IAA-glu synthetase. iaglu.

BAA36423.1 AB013598 *Verbena x hybrida*
UDP-glucose:anthocyanin 5-O-glucosyltransferase. HGT8.

AAF17077.1 AF199453 *Sorghum bicolor*
UDP-glucose glucosyltransferase.
UDP-glucose:p-hydroxymandelonitrile-o- glucosyltransferase.

CAA54558.1 X77369 *Solanum melongena*
glycosyl transferase. GT.

AAK16175.1 AC079887 *Oryza sativa*
putative glucosyltransferase. OSJNBa0040E01.15.

CAA81057.1 Z25802 *Petunia x hybrida*
UDP rhamnose: anthocyanidin-3-glucoside
rhamnosyltransferase.

CAA50377.1 X71060 *Petunia x hybrida*
anthocyanin: rhamnosyltransferase. rt.

CAA50376.1 X71059 *Petunia x hybrida*
anthocyanin 3 glucoside: rhamnosyltransferase. rt.

AAK16181.1 AC079887 *Oryza sativa*
putative glucosyltransferase. OSJNBa0040E01.16.

AAK16178.1 AC079887 *Oryza sativa*
putative glucosyltransferase. OSJNBa0040E01.5.

AAD21086.1 AF127218 *Forsythia x intermedia*
adds glucose residue to position 3 of flavonoid compounds.
flavonoid 3-O-glucosyltransferase. UFGT.

BAA89008.1 AB027454 *Petunia x hybrida*
anthocyanidin 3-O-glucosyltransferase. PGT8.

SEQ ID NO:1962

CAA65580.1 X96784 *Nicotiana tabacum*
cytochrome P450. hsr515.

CAA64635.1 X95342 *Nicotiana tabacum*
cytochrome P450. hsr515. hypersensitivity-related gene.

AAG44132.1 AF218296 *Pisum sativum*
cytochrome P450. P450 isolog.

AAG49299.1 AF313489 *Callistephus chinensis*
flavonoid 3',5'-hydroxylase.

BAA03438.1 D14588 *Petunia x hybrida*
flavonoid-3',5'-hydroxylase. Hfl.

AAC32274.1 AF081575 *Petunia x hybrida*
flavonoid 3',5'-hydroxylase. Hfl. P450 enzyme.

CAA50442.1 X71130 *Petunia x hybrida*
P450 hydroxylase. PET 1.

CAA80266.1 Z22545 *Petunia x hybrida*
flavonoid 3',5'-hydroxylase.

AAG49315.1 AF315465 *Pelargonium x hortorum*
flavonoid 3'-hydroxylase.

AAG49298.1 AF313488 *Callistephus chinensis*
putative flavonoid 3'-hydroxylase.

AAB17562.1 U72654 *Eustoma grandiflorum*
flavonoid 3'5'-hydroxylase. F3'5'H. cytochrome P450; CYP75.

BAB20076.1 AB012925 *Torenia hybrida*
flavonoid 3',5'-hydroxylase. F3'5'H.

AAG14961.1 AF214007 *Brassica napus*
cytochrome p450-dependent monooxygenase. BNF5H1.

CAC26920.1 AJ295586 *Arabidopsis lyrata* subsp. *petraea*
ferulate-5-hydroxylase. fah1.

AAG14962.1 AF214008 *Brassica napus*
cytochrome p450-dependent monooxygenase. BNF5H2.

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- 15 All publications, patents and patent applications are incorporated herein by reference.
While in the foregoing specification this invention has been described in relation to certain preferred embodiments thereof, and many details have been set forth for purposes of illustration, it will be apparent to those skilled in the art that the invention is susceptible to additional embodiments and that certain of the details described herein may be varied
20 considerably without departing from the basic principles of the invention.

WHAT IS CLAIMED IS:

1. A method to identify at least one gene involved in plant resistance or response to infection by at least one pathogen comprising:
 - 5 a) determining or detecting plant gene expression in an incompatible interaction; and
 - b) identifying at least one gene whose expression is significantly altered in the incompatible interaction relative to expression of the at least one gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to infection by a pathogen, or in a corresponding compatible interaction.
- 10 2. A method to identify at least one gene involved in plant resistance or response to infection by at least one pathogen comprising:
 - a) determining or detecting plant gene expression in a compatible interaction; and
 - 15 b) identifying at least one gene whose expression is significantly altered in the compatible interaction relative to expression of the at least one gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to infection by a pathogen, or in a corresponding incompatible interaction.
- 20 3. The method of claim 1 or 2 wherein the compatible interaction is between a plant having a resistance gene and a pathogen lacking a corresponding avirulence gene, a plant lacking a resistance gene to a pathogen having a corresponding avirulence gene, or a plant lacking a resistance gene and a pathogen lacking a corresponding avirulence gene.
- 25 4. The method of claim 1 or 2 wherein expression of the at least one gene is upregulated in response to infection.
5. The method of claim 1 or 2 wherein expression of the at least one gene is downregulated in response to infection.
- 30 6. The method of claim 1 or 2 wherein the at least one gene encodes a polypeptide that is substantially similar to a polypeptide encoded by an open reading frame comprising one of SEQ ID NOs:1-953, 1954-1966, 2000-2129 or 2662-4737.

7. The method of claim 1 or 2 wherein the at least one gene comprises an open reading frame comprising one of SEQ ID NOs:1-953, 1954-1966, 2000-2129 or 2662-4737.
8. The method of claim 1 or 2 wherein the pathogen is a bacterium.
- 5 9. The method of claim 1 or 2 wherein the pathogen is a fungus.
- 10 10. The method of claim 1 or 2 wherein the pathogen is a virus.
- 11 11. The method of claim 1 or 2 wherein gene expression is detected or determined using a gene chip, a cDNA array, cDNA-AFLP, or differential display PCR
12. The method of any one of claims 1 to 6 or 8 to 11 wherein the plant is a dicot.
- 15 13. The method of any one of claims 1 to 6 or 8 to 11 wherein the plant is a monocot.
14. The method of any one of claims 1 to 13 further comprising isolating the at least one gene or a portion thereof which includes the open reading frame or promoter for the gene.
- 20 15. A method to identify at least one gene, the expression of which is altered by pathogen infection in a wild-type plant relative to a plant having a mutation that decreases jasmonic acid or ethylene-dependent signaling, comprising:
 - a) contacting a plurality of isolated nucleic acid samples on a solid substrate each comprising isolated nucleic acid with a probe comprising plant nucleic acid
25 corresponding to RNA from a wild-type plant infected with the pathogen, so as to form a complex, wherein each sample comprises a plurality of oligonucleotides corresponding to at least a portion of one plant gene; and
 - b) comparing complex formation in a) with complex formation between a second plurality of isolated nucleic acid samples on a solid substrate with a second probe comprising
30 nucleic acid corresponding to RNA from the plant having the mutation and infected with the pathogen, so as to identify a gene, the expression of which is altered by pathogen infection in a wild-type plant relative to the mutant plant.

16. A method to identify at least one gene, the expression of which is altered by pathogen infection in a wild-type plant relative to a plant having a mutation in a gene that interferes with salicylic acid dependent signaling, comprising:
- 5 a) contacting a plurality of isolated nucleic acid samples on a solid substrate each comprising isolated nucleic acid with a probe comprising plant nucleic acid corresponding to RNA from a wild-type plant infected with the pathogen, so as to form a complex, wherein each sample comprises a plurality of oligonucleotides corresponding to at least a portion of one plant gene; and
- 10 b) comparing complex formation in a) with complex formation between a second plurality of isolated nucleic acid samples on a solid substrate with a second probe comprising nucleic acid corresponding to RNA from the plant having a mutation and infected with the pathogen, so as to identify a gene, the expression of which is altered by pathogen infection in a wild-type plant relative to the mutant plant.
- 15 17. A method to identify at least one gene, the expression of which is altered by pathogen infection in a wild-type plant relative to a plant having a mutation that results in enhanced susceptibility to bacterial infection, comprising:
- 20 a) contacting a plurality of isolated nucleic acid samples on a solid substrate each comprising isolated nucleic acid with a probe comprising plant nucleic acid corresponding to RNA from a wild-type plant infected with the pathogen, so as to form a complex, wherein each sample comprises a plurality of oligonucleotides corresponding to at least a portion of one plant gene; and
- 25 b) comparing complex formation in a) with complex formation between a second plurality of isolated nucleic acid samples on a solid substrate with a second probe comprising nucleic acid corresponding to RNA from the plant having a mutation and infected with the pathogen, so as to identify a gene, the expression of which is altered by pathogen infection in a wild-type plant relative to the mutant plant.
- 30 18. A method to identify at least one gene, the expression of which is altered by infection with at least one virus, comprising:
- a) contacting a plurality of isolated nucleic acid samples on a solid substrate each comprising isolated nucleic acid with a probe comprising plant nucleic acid corresponding to RNA from a wild-type plant infected with a virus, so as to form a

- complex, wherein each sample comprises a plurality of oligonucleotides corresponding to at least a portion of one plant gene; and
- b) comparing complex formation in a) with complex formation between a second plurality of isolated nucleic acid samples on a solid substrate with a second probe comprising nucleic acid corresponding to RNA from an uninfected plant, so as to identify a gene, the expression of which is altered by virus infection.
- 5
19. A method to identify at least one gene, the expression of which is altered by infection with at least one pathogen comprising:
- 10 a) contacting a plurality of isolated nucleic acid samples on a solid substrate each comprising isolated nucleic acid with a probe comprising plant nucleic acid corresponding to RNA from an incompatible interaction so as to form a complex, wherein each sample comprises a plurality of oligonucleotides corresponding to at least a portion of one plant gene; and
- 15 b) comparing complex formation in a) with complex formation between a second plurality of isolated nucleic acid samples on a solid substrate with a second probe comprising nucleic acid corresponding to RNA from a corresponding compatible interaction so as to identify a gene, the expression of which is altered by the pathogen.
- 20 20. The method of any one of claims 15 to 19 wherein the at least one gene is upregulated.
21. The method of any one of claims 15 to 19 wherein the at least one gene is downregulated.
22. The method of any one of claims 15 to 19 wherein the gene which is identified encodes a polypeptide that is substantially similar to a polypeptide encoded by an open reading frame comprising any one of SEQ ID NOs:1-953, 1954-1966, 2000-2129 or 2662-4737.
- 25
23. The method of any one of claims 15 to 19 wherein the probes comprise nucleic acid from a dicot.
- 30
24. The method of any one of claims 15 to 19 wherein the probes comprise nucleic acid from a cereal plant.

25. The method of any one of claims 15 to 19 wherein the probes comprise nucleic acid from a monocot.
26. The method of any one of claims 15 to 19 further comprising identifying the promoter for the at least one gene.
27. An isolated polynucleotide comprising a plant nucleotide sequence that alters transcription of an operatively linked nucleic acid segment in a plant cell after pathogen infection, which plant nucleotide sequence is from a gene encoding a polypeptide that is substantially similar to a polypeptide encoded by a gene comprising a promoter selected from the group consisting of SEQ ID NOs:2137-2661 or SEQ ID NOs:4738-6813.
28. An isolated polynucleotide comprising a plant nucleotide sequence that alters transcription of an operatively linked nucleic acid segment in a plant cell after pathogen infection, which plant nucleotide sequence hybridizes under high stringency conditions to the complement of any one of SEQ ID NOs:2137-2661 or SEQ ID NOs:4738-6813.
29. An isolated polynucleotide comprising a plant nucleotide sequence that alters transcription of an operatively linked nucleic acid segment in a plant after pathogen infection, which plant nucleotide sequence hybridizes under very high stringency conditions to the complement of any one of SEQ ID NOs:2137-2661 or SEQ ID NOs:4738-6813.
30. An isolated polynucleotide comprising a plant nucleotide sequence that directs transcription of an operatively linked nucleic acid segment in a plant cell, which plant nucleotide sequence is selected from the group consisting of SEQ ID NOs:2137-2661 and or SEQ ID NOs:4738-6813.
31. The polynucleotide of any one of claims 27 to 30 wherein the plant nucleotide sequence is 25 to 2000 nucleotides in length.
32. The polynucleotide of any one of claims 27 to 30 wherein the plant nucleotide sequence has at least 90% nucleotide sequence identity to one of SEQ ID NOs:2137-2661 or SEQ ID NOs:4738-6813.

33. The polynucleotide of any one of claims 27 to 30 wherein the plant nucleotide sequence has at least 98% nucleotide sequence identity to one of SEQ ID NOs:2137-2661 or SEQ ID NOs:4738-6813.
- 5
34. The polynucleotide of any one of claims 27 to 29 and 31 to 33 wherein the plant nucleotide sequence is from a dicot.
35. The polynucleotide of any one of claims 26 to 29 and 31 to 33 wherein the plant nucleotide sequence is from a monocot.
- 10
36. The polynucleotide of any one of claims 26 to 29 and 31 to 33 wherein the plant nucleotide sequence is a maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat sequence.
- 15
37. The polynucleotide of any one of claims 27 to 36 which comprises a TATA box, a CAAT box, or both.
38. A composition comprising the polynucleotide of any one of claims 27 to 37.
- 20
39. A recombinant vector comprising the polynucleotide of any one of claims 27 to 38.
40. The vector of claim 39 which is selected from the group consisting of a plasmid, phagemid, cosmid, virus, F-factor and phage.
- 25
41. An expression cassette comprising the polynucleotide of any one of claims 27 to 37 operatively linked to an open reading frame.
42. The expression cassette of claim 41 operably linked to other suitable regulatory sequences.
- 30
43. The expression cassette of claim 41 wherein the open reading frame is in an antisense orientation relative to the nucleotide sequence which alters transcription.

44. The expression cassette of claim 41 wherein the open reading frame is in a sense orientation relative to the nucleotide sequence which alters transcription.
45. A recombinant vector comprising the expression cassette of claim 41.
- 5
46. The vector of claim 45 wherein the vector is selected from the group consisting of a plasmid, phagemid, cosmid, virus, F-factor or phage.
47. A host cell comprising the expression cassette of claim 41.
- 10
48. The host cell of claim 47 wherein the cell is selected from the group consisting of a yeast, a bacterium, a cereal plant cell, and an *Arabidopsis* cell.
49. A plant cell containing the expression cassette of claim 41.
- 15
50. The plant cell of claim 49 which is a monocot cell.
51. The plant cell of claim 49 which is a dicot cell.
- 20
52. A transformed plant, the genome of which is augmented with the expression cassette of claim 41.
53. A transformed plant comprising transformed plant cells, which cells contain the expression cassette of claim 41.
- 25
54. The transformed plant of claim 52 or 53 which is a dicot.
55. The transformed plant of claim 52 or 53 which is a monocot.
- 30
56. The transformed plant of claim 52 or 53 which is selected from the group consisting of maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice, wheat and *Arabidopsis*.

57. A method for augmenting a plant genome, comprising:
- a) contacting plant cells with the expression cassette of claim 41 so as to yield a transformed plant cell; and
 - b) regenerating the transformed plant cell to provide a differentiated transformed plant,
5 wherein the differentiated transformed plant expresses the open reading frame in the cells of the plant.
58. A method to alter the phenotype of a plant cell comprising: introducing the expression cassette of claim 41 into a plant cell and expressing that open reading frame in the cell so
10 as to alter a characteristic of that cell relative to a plant cell that does not comprise the expression cassette.
59. The method of claim 57 or 58 wherein the plant cell is a dicot cell.
- 15 60. The method of claim 57 or 58 wherein the plant is a monocot cell.
61. The method of claim 57 or 58 wherein the plant cell a cereal cell.
62. The method of claim 57 or 58 wherein the plant cell is selected from the group consisting
20 of a cell of maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice, wheat and *Arabidopsis*.
63. The method of claim 57 or 58 wherein the open reading frame is in an antisense orientation relative to the nucleotide sequence which alters transcription.
25
64. The method of claim 57 or 58 wherein the expression inhibits transcription or translation of endogenous plant nucleic acid sequences corresponding to the open reading frame.
65. The method of claim 57 or 58 wherein the open reading frame is in a sense orientation
30 relative to the nucleotide sequence which alters transcription.
66. The method of claim 57 wherein the open reading frame is expressed in an amount that is greater than the amount in a plant which does not comprise the expression cassette.

67. The method of claim 57 or 58 wherein the open reading frame encodes a protein.
68. The method of claim 67 wherein the protein encodes a regulatory product.
- 5 69. The method of claim 67 wherein the expression of the open reading frame confers insect resistance, bacterial resistance, fungal resistance, viral resistance, or nematode resistance.
70. A transformed plant prepared by the method of claim 57.
- 10 71. A product of the plant of claim 70 which comprises the expression cassette or the gene product encoded by the open reading frame.
72. The product of claim 71 which is selected from the group consisting of a seed, fruit,
15 vegetable, transgenic plant, and a progeny plant.
73. A computer-readable medium having stored thereon a data structure comprising:
a) a nucleic acid molecule that has at least 70% nucleic acid sequence identity to a
nucleotide molecule selected from the group consisting of SEQ ID NOs:1-953, 2137-
20 2661, 1954-1966, 2000-2129, 2662-4737, 4738-6813 or the complement thereof; and
b) a module receiving the nucleic acid molecule which compares the nucleic acid
sequence of the molecule to at least one other nucleic acid sequence.
74. The computer readable medium of claim 73 wherein the medium is selected from the
25 group consisting of magnetic tape, optical disk, CD-ROM, random access memory,
volatile memory, non-volatile memory and bubble memory.
75. A computer-readable medium having stored thereon computer executable instructions for
performing a method comprising:
30 a) receiving a nucleic acid molecule having at least 70% nucleic acid sequence identity to
a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-953, 2137-
2661, 1954-1966, 2000-2129, 2662-4737, 4738-6813 or the complement thereof; and

b) comparing the nucleic acid sequence of the molecule to at least one other nucleic acid sequence.

- 5 76. The computer readable medium of claim 75 wherein the medium is selected from the group consisting of magnetic tape, optical disk, CD-ROM, random access memory, volatile memory, non-volatile memory and bubble memory.
- 10 77. The computer readable medium of any one of claims 73 to 76 wherein the nucleotide sequence is not SEQ ID NOs. 1-208, 210-215, 217-261, 263-266, 268-316, 318-385, 387-424, 426-439, 441-799, or 801-953.
- 15 78. A method to confer resistance or tolerance to a plant to a pathogen, comprising:
a) contacting plant cells with an expression cassette comprising a polynucleotide encoding a polypeptide that is substantially similar to a polypeptide encoded by an open reading frame comprising any one of SEQ ID NOs:1-953, 1954-1966, 2000-2129 or 2662-4737 so as to yield transformed cells; and
20 b) regenerating the transformed plant cells to provide a differentiated transformed plant, wherein the differentiated transformed plant expresses the polynucleotide in the cells of the plant in an amount effective to confer resistance or tolerance to the plant to a pathogen relative to a corresponding plant which does not comprise the expression cassette.
- 25 79. The method of claim 78 wherein the polynucleotide hybridizes under moderate stringency conditions to the complement of any one of SEQ ID NOs:1-953, 1954-1966, 2000-2129 or 2662-4737.
80. The method of any one of claims 78 to 79 wherein the cells are monocot cells.
81. The method of any one of claims 78 to 79 wherein the cells are dicot cells.
- 30 82. The method of claim 78 wherein the open reading frame encodes a DNA binding protein, hormone response protein, membrane protein, metabolic protein, transposon, receptor/kinase, phosphatase, stress protein, cell wall protein, lipid transfer protein, heat

shock protein, protein processing protein, RNA processing protein, non-cell wall structural protein or a non-kinase signaling protein.

83. A transformed plant prepared by the method of any one of claims 78 to 82.
- 5 84. A seed of the plant of claim 83.
85. A progeny plant of the plant of claim 83.
- 10 86. A method to identify a plant cell infected with a pathogen, comprising:
- a) contacting isolated nucleic acid obtained from a plant cell suspected of being infected with a pathogen with at least one oligonucleotide under conditions effective to specifically amplify a nucleotide sequence corresponding to one of SEQ ID NOs:1-953, 1954-1966, 2000-2129 or 2662-4737 or a portion thereof, so as to yield an amplified
 - 15 product; and
 - b) detecting or determining the presence or amount of the amplified product, wherein the presence or amount of the amplified product is indicative of pathogen infection.
87. A method to identify a plant cell infected with a pathogen, comprising:
- 20 a) contacting a sample comprising polypeptides obtained from a plant cell suspected of being infected with a pathogen with an agent that specifically binds to a polypeptide that is substantially similar to a polypeptide encoded by an open reading frame comprising one of SEQ ID NOs:1-953, 1954-1966, 2000-2129 or 2662-4737 so as to form a complex, wherein the; and
 - 25 b) detecting or determining the presence or amount of the complex, wherein the presence or amount of the complex is indicative of pathogen infection.
88. A method to identify a plant cell infected with a pathogen, comprising:
- a) contacting nucleic acid obtained from a plant cell suspected of being infected with a
 - 30 pathogen with a probe corresponding to a sequence selected from the group consisting of SEQ ID Nos. 1-953, 1954-1966, 2000-2129 or 2662-4737 or a portion thereof, under stringent hybridization conditions to form a duplex, and

- b) detecting or determining the presence or amount of the duplex, wherein the presence of a duplex is indicative of infection.

89. A method for marker-assisted breeding to select for plants having altered
5 resistance to a pathogen comprising:
a) contacting plant DNA or cDNA with a probe comprising a sequence selected from the
group consisting of SEQ ID Nos. 1-953, 1954-1966, 2000-2129 or 2662-4737 or a
portion thereof which hybridizes under moderate stringency conditions to a gene
corresponding to one of of SEQ ID Nos. 1-953, 1954-1966, 2000-2129 or 2662-4737
10 so as to form a duplex; and
b) detecting or determining the presence or amount of the duplex, wherein the amount or
presence of the duplex is indicative of the presence of a gene, the expression of which
alters the resistance of the plant to a pathogen.

15

INTERNATIONAL SEARCH REPORT

International Application No

PCT/IB 01/01105

A. CLASSIFICATION OF SUBJECT MATTER
 IPC 7 C12N15/29 C12N15/82 C12Q1/68 A01H5/00 G06F17/00
 C07K14/415

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
 IPC 7 C07K C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, BIOSIS, MEDLINE, SEQUENCE SEARCH

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	SCHENK P M ET AL: "Coordinated plant defense responses in Arabidopsis revealed by microarray analysis" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, NATIONAL ACADEMY OF SCIENCE. WASHINGTON, US, vol. 97, no. 21, 10 October 2000 (2000-10-10), pages 11655-11660, XP002153163. ISSN: 0027-8424 the whole document	1-5, 8-21, 23-26
X	WO 97 49822 A (CIBA GEIGY AG ;ELLIS DANIEL MURRAY (US); FRIEDRICH LESLIE BETHARDS) 31 December 1997 (1997-12-31) the whole document	1-5, 8-21, 23-26

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance
 "E" earlier document but published on or after the international filing date
 "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
 "O" document referring to an oral disclosure, use, exhibition or other means
 "P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
 "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
 "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
 "&" document member of the same patent family

Date of the actual completion of the international search

9 July 2002

Date of mailing of the international search report

25. 09. 2002

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INTERNATIONAL SEARCH REPORT

International Application No
PCT/IB 01/01105

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 01 07603 A (TUZUN SADIK ;UNIV AUBURN (US); ABDULLAH MALIKAH (US); SINGH NAREND) 1 February 2001 (2001-02-01) the whole document	1-5, 8-21, 23-26
X	EP 1 033 405 A (CERES INC) 6 September 2000 (2000-09-06)	73-76, 78-86, 88,89
A	page 1 -page 26 see SEQ IN NO: 38097 page 325 -page 341; claims 1-34 -----	6,7,22

INTERNATIONAL SEARCH REPORT

International application No.
PCT/IB 01/01105

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claims Nos.: 87
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☒ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
Claims 1-26, 73-89 partially.

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box 1.2

Claims Nos.: 87

Present claim 87 relates to a product/compound defined by reference to a desirable characteristic or property, namely an agent that binds to a polypeptide encoded by an open reading frame.

The claims cover all products/compounds having this characteristic or property, whereas the application provides support within the meaning of Article 6 PCT and/or disclosure within the meaning of Article 5 PCT for only a very limited number of such products/compounds. In the present case, the claims so lack support, and the application so lacks disclosure, that a meaningful search over the whole of the claimed scope is impossible. Independent of the above reasoning, the claims also lack clarity (Article 6 PCT). An attempt is made to define the product/compound by reference to a result to be achieved. Again, this lack of clarity in the present case is such as to render a meaningful search over the whole of the claimed scope impossible. Consequently, no search has been carried out.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: claims 1-26, 73-89 partially

A method to identify at least one gene involved in plant resistance or response to infection by at least one pathogen wherein the gene encodes a polypeptide encoded by an open reading frame comprising SEQ ID NO: 1. A method to identify at least one gene, the expression of which is altered by pathogen infection, a computer-readable medium, a method to confer resistance or tolerance to a plant, a transformed plant, a seed, a method to identify a plant cell infected with a pathogen, a method for marker-assisted breeding comprising said nucleic acid.

Invention 2-3173: claims 1-26, 73-89 partially

same as invention 1 but comprising a gene in the order as given in claim 6 (invention 2 is limited to SEQ ID NO: 2 and invention 3173 is limited to SEQ ID NO: 4737).

Invention 3174: claims 26-77 partially

An isolated polynucleotide comprising a plant nucleotide sequence that alters transcription of an operatively linked nucleic acid comprising SEQ ID NO: 2137. A composition, a vector, an expression cassette, a host cell, a plant cell, a transformed plant, a method for augmenting a plant genome, a method to alter the phenotype of a plant cell, a computer-readable medium comprising said polynucleotide.

Invention 3174-5774: claims 26-77 partially

same as invention 3173 but comprising a promoter sequence in the order as given in claim 27 (invention 3174 comprises SEQ ID NO: 2138 and invention 5774 comprises SEQ ID NO: 6813).

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/IB 01/01105

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Form PCT/ISA/210 (patent family annex) (July 1992)